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OM protein - protein search, using sw model

Run on: July 27, 2004, 12:01:11 ; Search time 52 Seconds
(without alignments)
130.407 Million cell updates/sec

Title: US-09-784-553C-19_COPY_29_52
Perfect score: 129
Sequence: 1 FRQPDVAVKLGPDYHKIKQPMW 24

Scoring table: BLOSUM62
Gapop 10.0 , Capext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	129	100.0	303	4 AAB95802	Aab95802 Human pro
2	129	100.0	754	2 AAY07027	Aay07027 Breast ca
3	129	100.0	801	7 ADC35076	Adc35076 Human bre
4	113	87.6	1937	4 ABB58985	Abb58985 Drosophil
5	110	85.3	140	4 AAU16619	Aau16619 Human nov
6	110	85.3	140	6 ABU5688	Abu5688 Human nov
7	110	85.3	235	6 AAU16205	Aau16205 Human nov
8	110	85.3	235	6 ABUS5275	Abu5275 Human nov
9	107	82.9	688	3 AAY57898	Aay57898 Human tra
10	107	82.9	1390	5 ABUS5152	Abu5152 Human NOV
11	100	77.5	513	4 ABB68341	Abb68341 Drosophil
12	96	74.4	947	2 AAU81168	Aau81168 Transcrip
13	96	74.4	947	2 AAY07114	Aay07114 WO9904265
14	93	72.1	124	3 AAB32659	Aab32659 Eucalyptu
15	92	71.3	714	4 ABB10109	Abb10109 Rice deri
16	88	68.2	293	3 AAB32946	Aab32946 Pinus rad
17	88	68.2	422	3 AAG41764	Aag41764 Arabidops
18	88	68.2	568	3 AAG41763	Aag41763 Arabidops
19	88	68.2	590	3 AAG41762	Aag41762 Arabidops
20	88	68.2	2414	2 AAR84882	Aar84882 Transcrip
21	88	68.2	2414	2 AAU40057	Aau40057 Cellular
22	88	68.2	2414	5 ABB06340	Abb06340 Human p30
23	88	68.2	2414	6 ABU03968	Abu03968 Human exp
24	88	68.2	2414	6 ABU03980	Abu03980 Human exp
25	88	68.2	2414	6 ABU03975	Abu03975 Human exp

26	88	68.2	2414	6 ABU03978	Abu03978 Human exp
27	88	68.2	2414	6 ABU03976	Abu03976 Human exp
28	88	68.2	2441	2 AAR79054	Aar79054 CREB bind
29	88	68.2	2441	2 AAU40058	Aau40058 Cellular
30	88	68.2	2441	3 AAY94252	Aay94252 Mouse nuc
31	88	68.2	2441	4 ABB44555	Abb44555 Mouse wou
32	88	68.2	2441	6 ABU03977	Abu03977 Human exp
33	88	68.2	2442	4 ABB44556	Abb44556 Human wou
34	88	68.2	2442	5 ABG95114	Abg95114 Human tra
35	88	68.2	2442	6 ABU03979	Abu03979 Human exp
36	88	68.2	2442	6 ABU03981	Abu03981 Human exp
37	88	68.2	2442	6 ABU03967	Abu03967 Human exp
38	88	68.2	2442	6 ABU03965	Abu03965 Human exp
39	86	66.7	330	6 ABR41589	Abr41589 Human DIT
40	86	66.7	494	3 AAG36673	Aag36673 Arabidops
41	86	66.7	521	3 AAG36672	Aag36672 Arabidops
42	86	66.7	573	6 ABR41326	Abr41326 Human DIT
43	86	66.7	620	3 AAG36671	Aag36671 Arabidops
44	86	66.7	3190	4 AAB84634	Aab84634 Amino aci
45	86	66.7	3275	4 ABB70437	Abb70437 Drosophil

ALIGNMENTS

RESULT 1
AAB95802
ID AAB95802 standard; protein; 303 AA.
XX
AC AAB95802;
XX
DT 26-JUN-2001 (first entry)
XX
DE Human protein sequence SEQ ID NO:18783.
XX
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy.
XX
OS Homo sapiens.
XX
PN EP1074617-A2.
XX
PD 07-FEB-2001.
XX
PF 28-JUL-2000; 2000EP-00116126.
XX
PR 29-JUL-1999; 95JP-00248036.
PR 27-AUG-1999; 95JP-00300253.
PR 11-JAN-2000; 2000JP-00118776.
PR 02-MAY-2000; 2000JP-00183767.
PR 09-JUN-2000; 2000JP-00241899.
XX (HELI-) HELIX RES INST.
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX WPI; 2001-318749/34.

Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
XX
PS Claim 8; SEQ ID NO 18783; 2537bp + Sequence Listing; English.
XX
CC The present invention describes primer sets for synthesizing 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dr primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 complementary sequences defined in the specification, where the complementary sequences comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end

CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in the
 CC specification. The primer sets can be used in antisense therapy and in
 CC gene therapy. The primers are useful for synthesising polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to AAH95893
 CC represent human amino acid sequences, and AAH13629 to AAH13632 represent
 CC present invention
 CC
 XX SQ Sequence 303 AA;

Query Match 100.0%; Score 129; DB 4; Length 303;
 Best Local Similarity 100.0%; Pred. No. 5.9e-12;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRQPVDAVKLGDPYHKIIKQPM 24
 DB 102 FRQPVDAVKLGDPYHKIIKQPM 125

RESULT 2
 AAY07027
 ID AAY07027 standard; protein; 754 AA.

AC AAY07027;
 DT 02-JUL-1999 (first entry)
 DE Breast cancer associated antigen precursor sequence.
 KW Cancer associated antigen; diagnosis; research; treatment; human;
 KW breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer;
 KW prostate cancer.

OS Homo sapiens.

PN WO9904265-A2.

PD 28-JAN-1999.

PF 15-JUL-1998; 98WO-US014679.

PR 17-JUL-1997; 97US-00896164.

PR 10-OCT-1997; 97US-0061599P.

PR 10-OCT-1997; 97US-0061765P.

PR 10-OCT-1997; 97US-00948705.

PR 11-OCT-1997; 97GB-00021697.

PR 22-JUN-1998; 98US-00102322.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Old LJ, Scanlan MJ, Stockert E, Gure A, Chen Y, Gout I;

PI O'hare M, Obata Y, Pfrendschuh M, Tureci O, Sahin U;

XX WPI; 1999-132448/11.

XX New isolated cancer associated nucleic acids and polypeptides - isolated
 PT using sera from cancer patients, used to develop products for the
 PT diagnosis, monitoring or treatment of cancers.

XX Disclosure; Page 404-405; 787pp; English.

XX The invention relates to a method for diagnosing a disorder characterised
 CC by expression of a human cancer associated antigen precursor coded for by
 CC a nucleic acid molecule (NAM). The method comprises: (a) contacting a
 CC biological sample isolated from a subject with an agent that specifically
 CC binds to the NAM, an expression product or a fragment of an expression

CC product complexed with an HLA molecule; and (b) determining the
 CC interaction between the agent and the NAM or the expression product as a
 CC determination of the disorder. The products and methods can be used in
 CC the diagnosis, monitoring, research, or treatment of conditions
 CC characterised by the expression of various cancer associated antigens.
 CC The invention provides nucleic acid sequences and encoded polypeptides
 CC which are cancer associated antigen precursors expressed in human breast
 CC cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and
 CC lung cancer

XX SQ Sequence 754 AA;

Query Match 100.0%; Score 129; DB 2; Length 754;

Best Local Similarity 100.0%; Pred. No. 1.7e-11;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRQPVDAVKLGDPYHKIIKQPM 24

DB 52 FRQPVDAVKLGDPYHKIIKQPM 75

RESULT 3

ADC35076

ID ADC35076 standard; protein; 801 AA.

AC ADC35076;

DT 18-DEC-2003 (first entry)

DE Human breast cancer antigen seq id 42.

XX breast cancer; breast cancer diagnosis; breast cancer antigen.

OS Homo sapiens.

PN US2003108888-A1.

PD 12-JUN-2003.

PF 15-MAY-2002; 2002US-00146473.

PR 15-MAY-2001; 2001US-0291150P.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Scanlan MJ, Gout I, Stockert E, Old LJ, Gure A, Chen Y;

DR WPI; 2003-829397/77.

DR N-PSDB; ADC35118.

XX Diagnosing breast cancer in subject by obtaining biological sample from
 PT subject, contacting sample with breast cancer-associated polypeptides,
 PT determining specific binding between polypeptides and agents in sample.

XX Example 2; SEQ ID NO 42; 173pp; English.

XX The invention describes a method of diagnosing breast cancer in subject
 CC comprising contacting biological sample from subject with at least two
 CC different breast cancer-associated polypeptides (I) encoded by nucleic
 CC acid molecules (II) comprising sequence chosen from 42 fully defined
 CC sequences as given in specification, determining specific binding between
 CC (I) and agents in sample, where presence of the binding is diagnostic for
 CC breast cancer. The method is useful for diagnosing breast cancer in a
 CC subject. The sample is blood, lymph node fluid or breast discharge fluid.
 CC This is the amino acid sequence of a breast cancer antigen.

XX SQ Sequence 801 AA;

Query Match 100.0%; Score 129; DB 7; Length 801;

Best Local Similarity 100.0%; Pred. No. 1.8e-11;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRQPVDAVKLGDPYHKIIKQPM 24

Db 99 FRQPDVAVKGLPDYHKIIKQPM 122

RESULT 4
ABB58985
ID ABB58985 standard; protein; 1937 AA.

XX AC ABB58985;
XX DT 26-MAR-2002 (first entry)

XX Drosophila melanogaster polypeptide SEQ ID NO 3747.

XX Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.

XX Drosophila melanogaster.

XX WO200171042-A2.

XX 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US009231.

XX 23-MAR-2000; 2000US-0191637P.

XX 11-JUL-2000; 2000US-00614150.

XX (PEKE) PE CORP NY.

XX Venter JC, Adams M, Li PWD, Myers EW;

XX WPI; 2001-656860/75.

XX N-PSDB; ABL03088.

XX New isolated nucleic acid detection reagent for detecting 1000 or more

XX genes from Drosophila and for elucidating cell signaling and cell-cell

XX interactions.

XX Disclosure; SEQ ID NO 3747; 2ipp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent

XX capable of detecting 1000 or more genes from Drosophila. The invention is

XX useful in developmental biology and in elucidating cell signalling and

XX cell-cell interactions in higher eukaryotes for the development of

XX insecticides, therapeutics and pharmaceutical drugs. The invention

XX discloses genomic DNA sequences (ABU16176-ABU30511), expressed DNA

XX sequences (ABU01840-ABU16175) and the encoded proteins (ABB57737-

XX ABB72072). The sequence data for this patent did not form part of the

XX printed specification, but was obtained in electronic format directly

XX from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 1937 AA;

Query Match 87.6%; Score 113; DB 4; Length 1937;

Best Local Similarity 87.5%; Pred. No. 1.8e-09;

Matches 21; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 1 FRQPDVAVKGLPDYHKIIKQPM 24

Db 59 FQQPDVAVKGLPDYHKIIKQPM 82

RESULT 5

AAU16619

ID AAU16619 standard; protein; 140 AA.

XX AC AAU16619;

XX 07-NOV-2001 (first entry)

XX Human novel secreted protein, Seq ID 1572.

KW Human; immunosuppressive; antiarthritic; antirheumatic; cytostatic;
KW cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective;
KW antibacterial; virucide; fungicide; ophthalmological; vulnerary;
KW secreted protein; rheumatoid arthritis; hyperproliferative disorder;
KW cardiovascular disorder; cardiac arrest; cerebrovascular disorder;
KW cerebral ischaemia; angiogenesis; nervous system disorder;
KW Alzheimer's disease; infection; ocular disorder; corneal infection;
KW wound healing; epithelial cell proliferation; skin ageing; food additive;
KW preservative; antiproliferative.

XX Homo sapiens.

XX WO200155322-A2.

XX 02-AUG-2001.

XX 17-JAN-2001; 2001WO-US001341.

XX 31-JAN-2000; 2000US-0179065P.

XX 04-FEB-2000; 2000US-0180628P.

XX 24-FEB-2000; 2000US-0184684P.

XX 02-MAR-2000; 2000US-0186350P.

XX 16-MAR-2000; 2000US-0189874P.

XX 17-MAR-2000; 2000US-0190076P.

XX 18-APR-2000; 2000US-0198123P.

XX 19-MAY-2000; 2000US-0205515P.

XX 07-JUN-2000; 2000US-0209457P.

XX 28-JUN-2000; 2000US-0214886P.

XX 30-JUN-2000; 2000US-0215135P.

XX 07-JUL-2000; 2000US-0216647P.

XX 07-JUL-2000; 2000US-0216880P.

XX 11-JUL-2000; 2000US-0217487P.

XX 11-JUL-2000; 2000US-0217496P.

XX 14-JUL-2000; 2000US-0218290P.

XX 26-JUL-2000; 2000US-0220963P.

XX 26-JUL-2000; 2000US-0220964P.

XX 14-AUG-2000; 2000US-0224518P.

XX 14-AUG-2000; 2000US-0224519P.

XX 14-AUG-2000; 2000US-0225213P.

XX 14-AUG-2000; 2000US-0225214P.

XX 14-AUG-2000; 2000US-0225266P.

XX 14-AUG-2000; 2000US-0225267P.

XX 14-AUG-2000; 2000US-0225268P.

XX 14-AUG-2000; 2000US-0225270P.

XX 14-AUG-2000; 2000US-0225447P.

XX 14-AUG-2000; 2000US-0225757P.

XX 14-AUG-2000; 2000US-0225758P.

XX 14-AUG-2000; 2000US-0225759P.

XX 18-AUG-2000; 2000US-0226279P.

XX 22-AUG-2000; 2000US-0226681P.

XX 22-AUG-2000; 2000US-0226688P.

XX 23-AUG-2000; 2000US-0227182P.

XX 23-AUG-2000; 2000US-0227009P.

XX 30-AUG-2000; 2000US-0228924P.

XX 01-SEP-2000; 2000US-0229287P.

XX 01-SEP-2000; 2000US-0229343P.

XX 01-SEP-2000; 2000US-0229344P.

XX 01-SEP-2000; 2000US-0229345P.

XX 05-SEP-2000; 2000US-0229509P.

XX 05-SEP-2000; 2000US-0229513P.

XX 06-SEP-2000; 2000US-0230437P.

XX 06-SEP-2000; 2000US-0230438P.

XX 08-SEP-2000; 2000US-0231242P.

XX 08-SEP-2000; 2000US-0231243P.

XX 08-SEP-2000; 2000US-0231244P.

XX 08-SEP-2000; 2000US-0231413P.

XX 08-SEP-2000; 2000US-0231414P.

XX 08-SEP-2000; 2000US-0232080P.

XX 08-SEP-2000; 2000US-0232081P.

XX 12-SEP-2000; 2000US-0231968P.

XX 14-SEP-2000; 2000US-0232397P.

XX 14-SEP-2000; 2000US-0232398P.

XX 14-SEP-2000; 2000US-0232399P.

PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236357P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
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PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249246P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 01-DEC-2000; 2000US-0250300P.
PR 01-DEC-2000; 2000US-0250310P.
PR 01-DEC-2000; 2000US-0250319P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-02556719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251898P.
PR 08-DEC-2000; 2000US-0251989P.
PR 11-DEC-2000; 2000US-0251990P.
PR 05-JAN-2001; 2001US-0259678P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-489783/53.
XX N-PSDB; AAS26606.
XX
XX New nucleic acid molecules encoding 461 human secreted proteins for
XX diagnosing, preventing, treating or ameliorating medical conditions and
XX used as food additives or preservatives.
XX
XX Claim 11; SEQ ID NO 1572; 980pp; English.
XX
XX The invention relates to isolated nucleic acid molecules and their
XX encoded secreted proteins. The nucleic acids and proteins are used to
XX prevent, treat or ameliorate a medical condition in e.g. humans, mice,
XX rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used
XX in diagnosing a pathological condition or susceptibility to a
XX pathological condition. Antibodies to the proteins can also be used in
XX alleviating symptoms associated with the disorders and in diagnostic
XX immunoassays e.g. radioimmunoassays or enzyme linked immunosorbent assays
XX (ELISA). Disorders which are diagnosed or treated include autoimmune
XX diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g.
XX neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac
XX arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis,
XX nervous system disorders e.g. Alzheimer's disease, infections caused by
XX bacteria, viruses and fungi and ocular disorders e.g. corneal infection,
XX and many other disorders listed in the specification. The polypeptides
XX can also be used to aid wound healing and epithelial cell proliferation,
XX to prevent skin aging due to sunburn, to maintain organs before
XX transplantation, for supporting cell culture of primary tissues, to
XX regenerate tissues and in chemotaxis. The polypeptides can also be used
XX as a food additive or preservative to increase or decrease storage
XX capabilities, fat content, lipid, protein, carbohydrate, vitamins,
XX minerals, cofactors and other nutritional components. The present
XX sequence represents a novel secreted protein of the invention. Note: The
XX sequence data for this patent did not form part of the printed
Query Match 85.3%; Score 110; DB 4; Length 140;
Best Local Similarity 83.3%; Pred. NO. 2.9e-09;
Matches 20; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 FRQPVDAVKLGLPDYHKIKQPM 24
DQ 33 FYQPVDAIKLNPDPYHKIKNPM 56
RESULT 6
ABU55688
ID ABU55688 standard; protein; 140 AA.
XX
XX AC ABU55688;
XX
XX DT 18-MAR-2003 (first entry)
XX
XX Human novel polypeptide #775.
XX
XX Human; neural disorder; immune system disorder; renal disorder;
XX muscular disorder; respiratory disease; reproductive disorder;
XX gastrointestinal disorder; pulmonary disorder; cardiovascular disorder;
XX hyperproliferative disorder; inflammatory disease; allergic reaction;
XX blood related disorder; cancer; immunosuppressive; antineoplastic;
XX cardiovascular; nephrotropic; cytostatic; antiallergic; thrombolytic;
XX haemostatic; antiarteriosclerotic.

XX OS Homo sapiens.
 XX PN US2002132753-A1.
 XX PD 19-SEP-2002.
 XX XX 17-JAN-2001; 2001US-00764864.
 XX 31-JAN-2000; 2000US-0179065P.
 PR 04-FEB-2000; 2000US-0180628P.
 PR 28-JUN-2000; 2000US-0214886P.
 PR 07-JUL-2000; 2000US-0216647P.
 PR 07-JUL-2000; 2000US-0216880P.
 PR 11-JUL-2000; 2000US-0217487P.
 PR 11-JUL-2000; 2000US-0217496P.
 PR 14-JUL-2000; 2000US-0218290P.
 PR 26-JUL-2000; 2000US-0220963P.
 PR 26-JUL-2000; 2000US-0220964P.
 PR 14-AUG-2000; 2000US-0224518P.
 PR 14-AUG-2000; 2000US-0224519P.
 PR 14-AUG-2000; 2000US-0225267P.
 PR 14-AUG-2000; 2000US-0225368P.
 PR 14-AUG-2000; 2000US-0225370P.
 PR 14-AUG-2000; 2000US-0225447P.
 PR 14-AUG-2000; 2000US-0225757P.
 PR 14-AUG-2000; 2000US-0225758P.
 PR 22-AUG-2000; 2000US-0226868P.
 PR 30-AUG-2000; 2000US-0228924P.
 PR 01-SEP-2000; 2000US-0229287P.
 PR 01-SEP-2000; 2000US-0229343P.
 PR 01-SEP-2000; 2000US-0229344P.
 PR 01-SEP-2000; 2000US-0229345P.
 PR 05-SEP-2000; 2000US-0229309P.
 PR 05-SEP-2000; 2000US-0229513P.
 PR 08-SEP-2000; 2000US-0231413P.
 PR 21-SEP-2000; 2000US-0234223P.
 PR 21-SEP-2000; 2000US-0234274P.
 PR 21-SEP-2000; 2000US-0234957P.
 PR 27-SEP-2000; 2000US-0235834P.
 PR 27-SEP-2000; 2000US-0236327P.
 PR 29-SEP-2000; 2000US-0236367P.
 PR 29-SEP-2000; 2000US-0236368P.
 PR 29-SEP-2000; 2000US-0236369P.
 PR 29-SEP-2000; 2000US-0236370P.
 PR 02-OCT-2000; 2000US-0236802P.
 PR 02-OCT-2000; 2000US-0237037P.
 PR 02-OCT-2000; 2000US-0237038P.
 PR 02-OCT-2000; 2000US-0237039P.
 PR 02-OCT-2000; 2000US-0237040P.
 PR 13-OCT-2000; 2000US-0239935P.
 PR 20-OCT-2000; 2000US-0240960P.
 PR 20-OCT-2000; 2000US-0241785P.
 PR 20-OCT-2000; 2000US-0241809P.
 PR 01-NOV-2000; 2000US-0244617P.
 PR 17-NOV-2000; 2000US-0249299P.
 PR 08-DEC-2000; 2000US-0251856P.
 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251869P.
 XX (ROSE/) ROSEN C A.
 PA (RUBE/) RUBEN S W.
 PA (BARA/) BARASH S C.
 XX Rosen CA, Ruben SM, Barash SC;
 FI WPI; 2003-147444/14.
 XX N-ESDB; ABX73947.
 DR
 XX New polypeptides and nucleic acids, useful in gene therapy for treating,
 PT inhibiting or preventing e.g. neural, immune system, muscular,
 PT respiratory, reproductive, gastrointestinal, pulmonary, cardiovascular or
 PT renal disorders.

XX PS Claim 11; SEQ ID NO 1572; 402pp; English.
 XX CC The invention relates to human novel polypeptides and their associated
 CC polynucleotides. The polypeptides and polynucleotides are useful in gene
 CC therapy for treating, inhibiting or preventing neural disorders, immune
 CC system disorders (e.g. systemic lupus erythematosus, rheumatoid arthritis
 CC and multiple sclerosis), muscular disorders, respiratory diseases (e.g.
 CC nasal vestibulitis, nasal polyps and sinusitis), reproductive disorders,
 CC gastrointestinal disorders, pulmonary disorders, cardiovascular disorders
 CC (e.g. congenital heart defects, Ebstein's anomaly and hypoplastic left
 CC heart syndrome), renal disorders (e.g. acute kidney failure and end-stage
 CC renal disease), hyperproliferative disorders (e.g. Hodgkin's disease and
 CC leukaemia), inflammatory diseases (e.g. septic shock, bursitis and
 CC appendicitis), allergic reactions and conditions (e.g. asthma), blood
 CC related disorders (e.g. thrombosis, atherosclerosis and myocardial
 CC infarction) and cancerous diseases. Sequences ABU54914-ABU55699 and
 CC ABU55748 represent human novel polypeptides of the invention
 XX SQ Sequence 140 AA;
 SQ
 Query Match 85.3%; Score 110; DB 6; Length 140;
 Best Local Similarity 83.3%; Pred. No. 2.5e-09;
 Matches 20; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 FRQPDVAVKGLGPDYHKIKQPM 24
 DB 33 FYQPDVAVKGLGPDYHKIKQPM 56
 RESULT 7
 AAU16206
 ID AAU16206 standard; protein; 235 AA.
 XX AC AAU16206;
 XX DT 07-NOV-2001 (first entry)
 XX DE Human novel secreted protein, Seq ID 1159.
 KW Human; immunosuppressive; antiarthritic; antirheumatic; cytostatic;
 KW cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective;
 KW antibacterial; virucide; fungicide; ophthalmological; vulnerary;
 KW secreted protein; rheumatoid arthritis; hyperproliferative disorder;
 KW cardiovascular disorder; cardiac arrest; cerebrovascular disorder;
 KW cerebral ischaemia; angiogenesis; nervous system disorder;
 KW Alzheimer's disease; infection; ocular disorder; corneal infection;
 KW wound healing; epithelial cell proliferation; skin ageing; food additive;
 KW preservative; antiproliferative.
 XX OS Homo sapiens.
 XX WO200155322-A2.
 XX PD 02-AUG-2001.
 XX PF 17-JAN-2001; 2001WO-US001341.
 XX 31-JAN-2000; 2000US-0179065P.
 PR 04-FEB-2000; 2000US-0180628P.
 PR 24-FEB-2000; 2000US-0184664P.
 PR 02-MAR-2000; 2000US-0186350P.
 PR 16-MAR-2000; 2000US-0189874P.
 PR 17-MAR-2000; 2000US-0190076P.
 PR 18-APR-2000; 2000US-0198123P.
 PR 19-MAY-2000; 2000US-0205515P.
 PR 07-JUN-2000; 2000US-0209467P.
 PR 28-JUN-2000; 2000US-0214886P.
 PR 30-JUN-2000; 2000US-0215135P.
 PR 07-JUL-2000; 2000US-0216647P.
 PR 07-JUL-2000; 2000US-0216880P.
 PR 11-JUL-2000; 2000US-0217487P.
 PR 11-JUL-2000; 2000US-0217496P.

PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226686P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234233P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239355P.
PR 13-OCT-2000; 2000US-0239357P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246533P.
PR 08-NOV-2000; 2000US-0246534P.
PR 08-NOV-2000; 2000US-0246535P.
PR 08-NOV-2000; 2000US-0246536P.
PR 08-NOV-2000; 2000US-0246537P.
PR 08-NOV-2000; 2000US-0246538P.
PR 08-NOV-2000; 2000US-0246539P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249246P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251475P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 11-DEC-2000; 2000US-0251990P.
PR 05-JAN-2001; 2001US-0254037P.
PR 05-JAN-2001; 2001US-02559678P.
(HUMA-) HUMAN GENOME SCI INC.
Rosen CA, Barash SC, Ruben SM;
WPI; 2001-489783/53.
N-FSDB; AAS26193.
New nucleic acid molecules encoding 461 human secreted proteins for
diagnosing, preventing, treating or ameliorating medical conditions and
used as food additives or preservatives.
Claim 11; SEQ ID NO 1159; 980pp; English.
The invention relates to isolated nucleic acid molecules and their
encoded secreted proteins. The nucleic acids and proteins are used to
prevent, treat or ameliorate a medical condition in e.g. humans, mice,
rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used
in diagnosing a pathological condition or susceptibility to a
pathological condition. Antibodies to the proteins can also be used in
alleviating symptoms associated with the disorders and in diagnostic
immunoassays e.g. radioimmunoassays or enzyme linked immunosorbent assays
(ELISA). Disorders which are diagnosed or treated include autoimmune
diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g.
neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac

XX AAY57898;
AC
XX
XX
DT 23-MAR-2000 (first entry)
XX
XX Human transmembrane protein HTMPN-22.
DE
XX
XX Human; transmembrane protein; HTMPN; diagnosis; immunospecific;
KW antiproliferative; neuroprotective; immune disorder;
KW antiproliferative; neuroprotective; immune disorder;
KW reproductive disorder; smooth muscle disorder; neurological disorder;
KW gastrointestinal disorder; developmental disorder;
KW cell proliferative disorder.
XX
XX Homo sapiens.
OS
XX
XX WO9961471-A2.
PN
XX
XX 02-DEC-1999.
PD
XX
XX 28-MAY-1999; 99WO-US011904.
PF
XX
XX 29-MAY-1998; 98US-0087260P.
PR
XX 02-JUL-1998; 98US-0091674P.
PR
XX 02-OCT-1998; 98US-0102854P.
PR
XX 24-NOV-1998; 98US-0109869P.
PR
XX
XX (INCY-) INCYTE PHARM INC.
PA
XX
XX Tang YT, Lal P, Hillman JL, Yue H, Guegler KJ, Corley NC;
PI Bandman O, Patterson C, Gorgone GA, Kaser MR, Baughn MR, Au-Young J;
PI
XX WPI; 2000-072605/06.
DR
XX N-PSDB; AAZ56719.
DR
XX
XX Proteins, polynucleotides, vectors, host cells and antibodies used to
PT diagnose, treat or prevent immune, reproductive, smooth muscle,
PT neurological, gastrointestinal, developmental and cell proliferative
PT disorders.
XX
XX Claim 1; Page 128-130; 229pp; English.
PS
XX
XX AAZ56698 to AAZ56776 encode AAY57877 to AAY57955 which represent human
CC transmembrane proteins designated HTMPN-1 to HTMPN-79, respectively. The
CC transmembrane protein have immunospecific, antiproliferative and
CC neuroprotective activities. The human transmembrane proteins
CC polynucleotides encoding them and other compositions and methods from the
CC present invention, can be used for the diagnosis, treatment or prevention
CC of immune, reproductive, smooth muscle, neurological, gastrointestinal,
CC developmental and cell proliferative disorders. The HTMPN's can be used
CC to treat or prevent disorders associated with a decreased expression or
CC activity of HTMPN
XX
XX Sequence 688 AA;
SQ
Query Match 82.9%; Score 107; DB 3; Length 688;
Best Local Similarity 83.3%; Pred. No. 4.7e-08;
Matches 20; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 1 PROPVDVKLGDPYKHIIQOPMD 24
Db 83 FQPPVDVKLNLPPYKIIKTPMD 106
RESULT 10
ABU65152
ID ABU65152 standard; protein; 1390 AA.
XX
XX ABU65152;
AC
XX
XX 20-MAY-2003 (first entry)
DT
XX
XX Human NOV79a protein.
DE
XX
XX

KW NOVX; cytostatic; cardiant; antiarteriosclerotic; antiasthmatic; cancer;
KW hypotensive; cardiomyopathy; bronchial asthma; gene therapy; vaccine;
KW human.
XX
XX Homo sapiens.
OS
XX
XX WO200272757-A2.
PN
XX
XX 19-SEP-2002.
PD
XX
XX 08-MAR-2002; 2002WO-US006908.
PF
XX
XX 08-MAR-2001; 2001US-0274101P.
PR
XX 08-MAR-2001; 2001US-0274194P.
PR
XX 08-MAR-2001; 2001US-0274251P.
PR
XX 08-MAR-2001; 2001US-0274322P.
PR
XX 09-MAR-2001; 2001US-0274849P.
PR
XX 12-MAR-2001; 2001US-0275235P.
PR
XX 13-MAR-2001; 2001US-0275578P.
PR
XX 13-MAR-2001; 2001US-0275579P.
PR
XX 13-MAR-2001; 2001US-0275601P.
PR
XX 14-MAR-2001; 2001US-0276000P.
PR
XX 16-MAR-2001; 2001US-0276776P.
PR
XX 19-MAR-2001; 2001US-0276994P.
PR
XX 20-MAR-2001; 2001US-0277239P.
PR
XX 20-MAR-2001; 2001US-0277321P.
PR
XX 20-MAR-2001; 2001US-0277377P.
PR
XX 21-MAR-2001; 2001US-0277919P.
PR
XX 22-MAR-2001; 2001US-0277833P.
PR
XX 23-MAR-2001; 2001US-0278152P.
PR
XX 26-MAR-2001; 2001US-0278894P.
PR
XX 27-MAR-2001; 2001US-0278999P.
PR
XX 27-MAR-2001; 2001US-0279036P.
PR
XX 28-MAR-2001; 2001US-0279344P.
PR
XX 30-MAR-2001; 2001US-0277338P.
PR
XX 30-MAR-2001; 2001US-0279959P.
PR
XX 30-MAR-2001; 2001US-0280233P.
PR
XX 02-APR-2001; 2001US-0280802P.
PR
XX 02-APR-2001; 2001US-0280822P.
PR
XX 02-APR-2001; 2001US-0280900P.
PR
XX 04-APR-2001; 2001US-0281194P.
PR
XX 13-APR-2001; 2001US-0283675P.
PR
XX 30-APR-2001; 2001US-0287424P.
PR
XX 02-MAY-2001; 2001US-0288066P.
PR
XX 03-MAY-2001; 2001US-0288342P.
PR
XX 03-MAY-2001; 2001US-0288528P.
PR
XX 15-MAY-2001; 2001US-0291190P.
PR
XX 16-MAY-2001; 2001US-0291099P.
PR
XX 16-MAY-2001; 2001US-0291240P.
PR
XX 30-MAY-2001; 2001US-0294485P.
PR
XX 31-MAY-2001; 2001US-0294889P.
PR
XX 31-MAY-2001; 2001US-0294899P.
PR
XX 18-JUN-2001; 2001US-0299027P.
PR
XX 19-JUN-2001; 2001US-0299303P.
PR
XX 19-JUN-2001; 2001US-0299310P.
PR
XX 30-JUL-2001; 2001US-0304354P.
PR
XX 31-JUL-2001; 2001US-0309198P.
PR
XX 16-AUG-2001; 2001US-0312903P.
PR
XX 10-SEP-2001; 2001US-0318462P.
PR
XX 12-SEP-2001; 2001US-0318770P.
PR
XX 27-SEP-2001; 2001US-0325430P.
PR
XX 27-SEP-2001; 2001US-0325681P.
PR
XX 18-OCT-2001; 2001US-0330380P.
PR
XX 31-OCT-2001; 2001US-0335301P.
PR
XX 14-NOV-2001; 2001US-0332172P.
PR
XX 14-NOV-2001; 2001US-0332271P.
PR
XX 14-NOV-2001; 2001US-0332272P.
PR
XX 14-NOV-2001; 2001US-0333184P.
PR
XX 14-NOV-2001; 2001US-0333272P.
PR
XX 21-NOV-2001; 2001US-0332094P.
PR
XX 03-DEC-2001; 2001US-0337426P.
PR
XX 03-DEC-2001; 2001US-0338092P.
PR
XX 04-DEC-2001; 2001US-0337185P.
PR

03-JAN-2002; 2002US-0345705P.
07-MAR-2002; 2002US-00092900.
(CURA-) CURAGEN CORP.
XX
PI Padigaru M, Svytek KA, Shenoy SG, Taupier RJ, Pena CE, Li L;
PI Zehrhusen BD, Gusev V, Ji W, Cornan L, Miller CE, Kekuda R;
PI Patturajan M, Gangoli E, Vernet CAM, Guo X, Tchernev V;
PI Fernandes ER, Casman SJ, Malyankar UM, Gerlach V, Liu Y, Anderson D;
PI Spaderna SK, Catterton E, Butgess C, Leite M, Zhong H, Alsobrook JP;
PI Lepley DM, Rieger DK;
XX WPI; 2002-723332/78.
DR N-PSDB; ABX97119.
XX
XX NOVX polypeptides and polynucleotides, useful for preventing or treating
PT a disorder associated with aberrant NOVX expression or activity e.g.,
PT cancer, hypertension, atherosclerosis, cardiomyopathy or bronchial
PT asthma.
XX
XX Claim 1; Page 323; 1103pp; English.
PS
XX This invention describes novel human NOVX polypeptides which have
CC cytostatic, cardiac, antiarteriosclerotic, antiasthmatic and hypotensive
CC activity. Pharmaceutical compositions comprising the NOVX proteins or
CC nucleic acid molecules or NOVX antibodies are useful for preventing or
CC treating a disorder associated with aberrant NOVX expression or activity
CC e.g. cancer, hypertension, atherosclerosis, cardiomyopathy or bronchial
CC asthma. The products of the invention can be used for gene therapy or in
CC a vaccine. ABU65041-ABU65218 represent the NOVX polypeptides encoded by
CC ABX97008-ABX97185
XX
XX Sequence 1390 AA;
SQ
Query Match 82.9%; Score 107; DB 5; Length 1390;
Best Local Similarity 83.3%; Pred. No. 1.1e-07;
Matches 20; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 FRQPVDAVKLGLPDYHKIIKQPM 24
|:|||||:|||||:|||||
DB 83 FQQPVDAVKLNLDPDYKIIKTPMD 106
|:|||||:|||||:|||||
RESULT 11
ABX968341
ID ID ABB68341 standard; protein; 513 AA.
XX
XX ABB68341;
AC
XX
XX
DT 26-MAR-2002 (first entry)
XX
XX Drosophila melanogaster polypeptide SEQ ID NO 31815.
DE
XX Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX
XX Drosophila melanogaster.
OS
XX WO200171042-A2.
XX
XX 27-SEP-2001.
PD
XX
XX 23-MAR-2001; 2001WO-US009231.
PF
XX 23-MAR-2000; 2000US-0191637P.
PR 11-JUL-2000; 2000US-00614150.
XX
XX (PEKE) PE CORP NY.
PA
XX Venter JC, Adams M, Li PWD, Myers EW;
PI WPI; 2001-658660/75.
XX
DR N-PSDB; ABX12444.
DR

XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions.
XX
XX Disclosure; SEQ ID NO 31815; 21pp + Sequence Listing; English.
PS
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 513 AA;
SQ
Query Match 77.5%; Score 100; DB 4; Length 513;
Best Local Similarity 66.7%; Pred. No. 4.4e-07;
Matches 16; Conservative 4; Mismatches 4; Indels 0; Gaps 0
QY 1 FRQPVDAVKLGLPDYHKIIKQPM 24
|:|||||:|||||:|||||
DB 63 FRHPVDSVSLGVDPDYHVVKHPMD 86
|:|||||:|||||:|||||
RESULT 12
AAW81168
ID ID AAW81168 standard; protein; 947 AA.
XX
XX AAW81168;
AC
XX
XX 05-MAR-1999 (first entry)
DT
XX
XX Transcriptional regulatory factor RING3.
DE
XX Human; transcriptional regulatory factor; RING3; TSB; cancer;
KW testis specific bromodomain; testicular cell proliferation.
XX
XX Homo sapiens.
OS
XX WO9848015-A1.
XX
XX 29-OCT-1998.
PD
XX
XX 17-APR-1998; 98WO-JP001782.
PF
XX
XX 18-APR-1997; 97JP-00116402.
PR
XX (CHUS) CHUGAI RES INST MOLECULAR MEDICINE INC.
PA
XX Jones MH;
XX
XX WPI; 1998-593658/49.
XX
XX N-PSDB; AAV68343.
XX
XX Transcriptional regulator gene containing bromodomain sequence - may be
PT expressed in testis tissue and is useful in treatment of cancer and other
PT proliferative disorders.
XX
XX Claim 1; Page 19-24; 42pp; Japanese.
PS
XX The present sequence represents the human transcriptional regulatory
CC factor RING3, which is isolated from testicular cells. RING3 contains a
CC testis specific bromodomain (TSB) which is expressed specifically in
CC testis tissue and also expressed in certain tumour lines. The transgenic
CC cells may be used to express RING3 which is a TSB expression protein. The
CC TSB expression product can be used in the treatment of cancer and other
CC proliferative disorders, and in screening of compounds for ability to
CC bind to it (e.g. for use as drugs by modulation of transcriptional
CC

CC regulation). DNA capable of hybridising to RING3 polynucleotides may be
 CC used for construction of probes and primers
 XX
 XX Sequence 947 AA;

Query Match 74.4%; Score 96; DB 2; Length 947;
 Best Local Similarity 75.0%; Pred. No. 3.8e-06;
 Matches 18; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 FRQPVDAVKLGLEDYHKKIKQPM 24
 Db 52 FRQPVDAVKLGLEDYHKKIKQPM 75

RESULT 13
 AAY07114
 ID AAY07114 standard; protein; 947 AA.

AC AAY07114;
 XX
 XX 02-JUL-1999 (first entry)
 DT
 XX
 XX WO9904265 Seq ID No: 685.
 DE
 XX
 XX Cancer associated antigen; diagnosis; research; treatment; human;
 KW breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer;
 KW prostate cancer.
 KW
 XX Homo sapiens.
 OS
 XX
 XX WO9904265-A2.
 PN
 XX
 XX 28-JAN-1999.
 PD
 XX
 XX 15-JUL-1998; 98WO-US014679.

XX 17-JUL-1997; 97US-00896164.
 PR 10-OCT-1997; 97US-00611599P.
 PR 10-OCT-1997; 97US-0061765P.
 PR 10-OCT-1997; 97US-00948705.
 PR 11-OCT-1997; 97GB-00021697.
 PR 22-JUN-1998; 98US-00102322.
 XX
 XX (LUDW-) LUDWIG INST CANCER RES.

XX Old Lu, Scanlan MJ, Stockert E, Gure A, Chen Y, Gout I;
 XX O'hare M, Obata Y, Pfrendschuh M, Tureci O, Sahin U;
 XX WPI; 1999-132448/11.

XX New isolated cancer associated nucleic acids and polypeptides - isolated
 XX using sera from cancer patients, used to develop products for the
 XX diagnosis, monitoring or treatment of cancers.

XX Disclosure; Page 728-730; 787pp; English.

XX The invention relates to a method for diagnosing a disorder characterised
 XX by expression of a human cancer associated antigen precursor coded for by
 XX a nucleic acid molecule (NAM). The method comprises: (a) contacting a
 XX biological sample isolated from a subject with an agent that specifically
 XX binds to the NAM, an expression product or a fragment of an expression
 XX product complexed with an HLA molecule; and (b) determining the
 XX interaction between the agent and the NAM or the expression product as a
 XX determination of the disorder. The products and methods can be used in
 XX the diagnosis, monitoring, research, or treatment of conditions
 XX characterised by the expression of various cancer associated antigens.
 XX The invention provides nucleic acid sequences and encoded polypeptides
 XX which are cancer associated antigen precursors expressed in human breast
 XX cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and
 XX lung cancer

XX Sequence 947 AA;

Query Match 74.4%; Score 96; DB 2; Length 947;
 Best Local Similarity 75.0%; Pred. No. 3.8e-06;
 Matches 18; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 FRQPVDAVKLGLEDYHKKIKQPM 24
 Db 52 FRQPVDAVKLGLEDYHKKIKQPM 75

RESULT 14
 AAB32659
 ID AAB32659 standard; protein; 124 AA.

XX AAB32659;

XX 25-JAN-2001 (first entry)

XX Eucalyptus grandis transcription factor protein sequence #117.

XX Plant; transcription factor; gene expression; eucalyptus; pine; acacia;
 KW poplar; sweetgum; teak; mahogany; bZIP; G-box binding factor;
 KW basic helix-loop-helix zipper; homeotic; homeodomain; homeobox; MADS;
 KW homeodomain zipper; LIM domain; AP2; EREBs; zinc finger domain;
 KW type 2 Cys2His2; CCAAT box element; MYB.

XX Eucalyptus grandis.

XX WO2000053724-A2.

XX 14-SEP-2000.

XX 09-MAR-2000; 2000WO-US006112.

XX 11-MAR-1999; 99US-00266513.

XX 18-AUG-1999; 99US-0149485P.

XX (GENE-) GENESIS RES & DEV CORP LTD.
 XX (FLET-) FLETCHER CHALLENGE FORESTS LTD.

XX Wood M, McGrath A, Shenk MA, Glenn M;

XX WPI; 2000-579369/54.

XX New isolated polynucleotide encoding a plant transcription factor for
 XX producing a plant e.g. a woody plant, preferably eucalyptus or pine,
 XX having modified gene expression or modified activity of a polypeptide.

XX Claim 8; Page 246; 747pp; English.

XX The present invention relates to novel plant transcription factors from
 XX Eucalyptus grandis or Pinus radiata. The present sequence is one such
 XX transcription factor. The transcription factor may be used to produce a
 XX plant having modified gene expression such as a woody plant e.g. a
 XX eucalyptus, pine, acacia, poplar, sweetgum, teak, or mahogany species or
 XX to modify the activity of a polypeptide in a plant. The transcription
 XX factors of the present invention are members from the following families
 XX of regulatory proteins: bZIP, bZIP family of G-box binding factors, basic
 XX helix-loop-helix zipper, homeotic/homeodomain/homeobox/MADS, homeodomain/
 XX zipper, LIM domain, AP2 and EREB, zinc finger domains of type 2
 XX Cys2His2, CCAAT box elements and MYB

XX Sequence 124 AA;

Query Match 72.1%; Score 93; DB 3; Length 124;
 Best Local Similarity 75.0%; Pred. No. 1.1e-06;
 Matches 18; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 FRQPVDAVKLGLEDYHKKIKQPM 24
 Db 44 FNTFVDAVGLGHDYHQIKNPMD 67

RESULT 15

ABB10109
ID ABB10109 standard; protein; 714 AA.
XX AC ABB10109;
XX DT 01-JUL-2002 (first entry)
XX DE Rice derived plant resistance protein#3.
XX KW Plant; resistance; cerebroside type elicitor; rice blight microbe.
XX OS Oryza sativa.
XX PN JP2000342262-A.
XX PD 12-DEC-2000.
XX PF 31-MAY-1999; 99JP-00153146.
XX PR 31-MAY-1999; 99JP-00153146.
XX PA (SHOK-) SHOKUBUTSU SOGYO SYSTEM KENKYUSHO KK.
XX DR WPI; 2001-268250/28.
XX DR N-PSDB; ABL56859.
XX PT New gene for giving acquired resistance to a plant and a method for
PT screening for it, comprising using a cerebroside type elicitor derived
PT from a rice blight microbe.
XX PS Claim 3; Page 14-16; 34pp; Japanese.
XX CC The invention relates to a gene encoding a protein giving acquired
CC resistance to a plant, and a method for screening for it using a
CC cerebroside type elicitor derived from a rice blight microbe. The new
CC gene can be used to give acquired resistance to a plant. The current
CC sequence represents a rice derived plant resistance protein
XX SQ Sequence 714 AA;
Query Match 71.3%; Score 92; DB 4; Length 714;
Best Local Similarity 70.8%; Pred. No. 1.2e-05;
Matches 17; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 FROPDAVKLGDPDYHKIKQPM 24
Db 187 FDSFVDAVKLNIPDYFQIIKKPM 210
Search completed: July 27, 2004, 12:07:14
Job time : 54 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 27, 2004, 11:58:16 ; Search time 18 Seconds
(without alignments)
68.835 Million cell updates/sec

Title: US-09-784-553C-19_COPY_29_52
Perfect score: 129
Sequence: 1 FRQPDVAVKLGPDYHKIIQKPM 24

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/prodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/prodata/2/iaa/5A_COMB.pep.*
4: /cgn2_6/prodata/2/iaa/5B_COMB.pep.*
5: /cgn2_6/prodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/prodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	129	100.0	65	1	US-08-227-536-5
2	129	100.0	65	5	PCT-US95-04682-5
3	129	100.0	754	4	US-09-392-714-20
4	110	85.3	726	4	US-09-392-714-21
5	107	82.9	722	4	US-09-392-714-22
6	96	74.4	947	4	US-09-418-780A-1
7	96	74.4	947	4	US-09-392-714-23
8	89	69.0	61	4	US-09-418-710-42
9	88	68.2	61	4	US-09-418-710-55
10	88	68.2	2414	1	US-08-227-536-2
11	88	68.2	2414	5	PCT-US95-04682-2
12	88	68.2	2441	1	US-08-194-468-2
13	88	68.2	2441	3	US-08-961-739-2
14	88	68.2	2441	4	US-09-514-247A-8
15	88	68.2	2442	4	US-09-686-316-2
16	88	68.2	2442	4	US-09-514-247A-10
17	86	66.7	65	1	US-08-227-536-6
18	86	66.7	65	5	PCT-US95-04682-6
19	61	47.3	65	1	US-08-227-536-3
20	61	47.3	65	1	US-08-227-536-4
21	61	47.3	65	5	PCT-US95-04682-3
22	61	47.3	65	5	PCT-US95-04682-4
23	58	45.0	59	4	US-09-418-710-51
24	58	45.0	238	4	US-09-257-179-80
25	58	45.0	1872	1	US-08-188-582-14
26	58	45.0	1872	1	US-08-646-715-14
27	58	45.0	1893	1	US-08-188-582-11

28	58	45.0	1893	1	US-08-646-715-11
29	56	43.4	11	4	US-09-418-780A-14
30	56	43.4	11	4	US-09-418-780A-22
31	55	42.6	65	1	US-08-227-536-8
32	55	42.6	65	5	PCT-US95-04682-8
33	53.5	41.5	21	4	US-09-257-179-85
34	53	41.1	59	4	US-09-418-710-40
35	52	40.3	59	4	US-09-418-710-39
36	52	40.3	740	4	US-09-107-532A-7211
37	52	40.3	1969	4	US-09-418-710-72
38	52	40.3	1972	4	US-09-418-710-21
39	49	38.0	59	4	US-09-418-710-58
40	49	38.0	59	4	US-09-418-710-50
41	49	38.0	1673	4	US-09-418-710-70
42	49	38.0	1674	4	US-09-418-710-1
43	48	37.2	59	4	US-09-418-710-41
44	48	37.2	59	4	US-09-418-710-53
45	47	36.4	274	4	US-09-134-000C-5795

ALIGNMENTS

RESULT 1
US-08-227-536-5
; Sequence 5, Application US/08227536
; Patent No. 5658784
; GENERAL INFORMATION:
; APPLICANT: Ecken, Richard
; APPLICANT: Ewen, Mark
; APPLICANT: Livingston, David
; TITLE OF INVENTION: NUCLEIC ACID, ENCODING TRANSCRIPTION
; TITLE OF INVENTION: FACTOR P300 AND USES OF P300
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes
; STREET: Ten Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/227,536
; FILING DATE: 14-APR-1994
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Ph.D., Kathleen A.
; REGISTRATION NUMBER: 34,380
; REFERENCE/DOCKET NUMBER: DPCI-308XX
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-2290
; TELEFAX: (617) 451-0313
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 65 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
US-08-227-536-5

Query Match 100.0%; Score 129; DB 1; Length 65;
Best Local Similarity 100.0%; Pred. No. 1.3e-13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FRQPDVAVKLGPDYHKIIQKPM 24

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Db      6 FRQPDVAVKLGDPYHKIIKQPM 29
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RESULT 2
PCT-US95-04682-5
; Sequence 5, Application PC/TUS9504682
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: NUCLEIC ACID ENCODING TRANSCRIPTION
; TITLE OF INVENTION: FACTOR P300 AND USES OF P300
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes
; STREET: Ten Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04682
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,536
; FILING DATE: 14-April-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Holliday C. Heine, Ph.D.
; REGISTRATION NUMBER: 34,346
; REFERENCE/DOCKET NUMBER: DFCI-308XQ999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-2290
; TELEFAX: (617) 451-0313
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 65 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; PCT-US95-04682-5

Query Match      100.0%; Score 129; DB 5; Length 65;
Best Local Similarity 100.0%; Pred. No. 1.3e-13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FRQPDVAVKLGDPYHKIIKQPM 24
Db      6 FRQPDVAVKLGDPYHKIIKQPM 29
|||||
RESULT 3
US-09-392-714-20
; Sequence 20, Application US/09392714A
; Patent No. 6686147
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Gure, Ali O.
; APPLICANT: Williamson, Barbara
; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: Cancer Associated Antigens and Uses
; FILE REFERENCE: L0461/7062
; CURRENT APPLICATION NUMBER: US/09/392,714A
; EARLIER FILING DATE: 1999-09-09
; SOFTWARE: FastSEQ for Windows Version 3.0
; NUMBER OF SEQ ID NOS: 30
; FILE REFERENCE: L0461/7062
; CURRENT APPLICATION NUMBER: US/09/392,714A
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; CURRENT FILING DATE: 1999-09-09
; EARLIER APPLICATION NUMBER: PCT/US98/14679
; EARLIER FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 754
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-392-714-20
Query Match      100.0%; Score 129; DB 4; Length 754;
Best Local Similarity 100.0%; Pred. No. 2.2e-12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FRQPDVAVKLGDPYHKIIKQPM 24
Db      52 FRQPDVAVKLGDPYHKIIKQPM 75
|||||
RESULT 4
US-09-392-714-21
; Sequence 21, Application US/09392714A
; Patent No. 6686147
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Gure, Ali O.
; APPLICANT: Williamson, Barbara
; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: Cancer Associated Antigens and Uses
; FILE REFERENCE: L0461/7062
; CURRENT APPLICATION NUMBER: US/09/392,714A
; EARLIER FILING DATE: 1999-09-09
; EARLIER APPLICATION NUMBER: PCT/US98/14679
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 726
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-392-714-21
Query Match      85.3%; Score 110; DB 4; Length 726;
Best Local Similarity 83.3%; Pred. No. 2.4e-09;
Matches 20; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      1 FRQPDVAVKLGDPYHKIIKQPM 24
Db      59 FYQPDVAVKLGDPYHKIIKQPM 82
|||||
RESULT 5
US-09-392-714-22
; Sequence 22, Application US/09392714A
; Patent No. 6686147
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Gure, Ali O.
; APPLICANT: Williamson, Barbara
; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: Cancer Associated Antigens and Uses
; FILE REFERENCE: L0461/7062
; CURRENT APPLICATION NUMBER: US/09/392,714A
; EARLIER FILING DATE: 1999-09-09
; EARLIER APPLICATION NUMBER: PCT/US98/14679
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 3.0
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; SEQ ID: NO 22
;
; LENGTH: 722
;
; TYPE: PRT
;
; ORGANISM: Homo sapiens
US-09-392-714-22

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Query_Match      82.9%; Score 107; DB 4; Length 722;
Best Local Similarity 83.3%; Pred. No. 7.2e-09;
Matches 20; Conservative 2; Mismatches 0; Gaps 0;
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```

RESULT 6
US-09-418-780A-1
; Sequence 1, Application US/09418780A
; Patent No. 6504009
; GENERAL INFORMATION:
; APPLICANT: Jones, Michael H.
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
; FILE REFERENCE: 06501-043001
; CURRENT APPLICATION NUMBER: US/09/418,780A
; CURRENT FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: PCT/JP98/01782
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: JAPAN 9/116402
; PRIOR FILING DATE: 1997-04-18
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 947
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-418-780A-1

```

```

Query Match      74.4%; Score 96; DB 4; Length 947;
Best_Local_Similarity 75.0%; Pred.No. 5.7e-07;
Matches 18; Conservative 3; Mismatches 0; Gaps 0;
QY      1 FRQPVDAVKLGLEFDYHKIKQFMD 24
      ::::|::|::|::|::|::|::|::|
Db      52 FORPVDVKLGLEFDYHTIIRKQFMD 75

```

```

RESULT 7
US-09-392-714-23
; Sequence 23, Application US/09392714A
; Patent No. 6686147
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Gure, Ali O.
; APPLICANT: Williamson, Barbara
; APPLICANT: Chen, Yao-Tsung
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: Cancer Associated Antigens and Uses
; TITLE OF INVENTION: Therefor
; FILE REFERENCE: L0461/7062
; CURRENT APPLICATION NUMBER: US/09/392,714A
; CURRENT FILING DATE: 1999-09-09
; EARLIER APPLICATION NUMBER: PCT/US98/14679
; EARLIER FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 947
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-392-714-23

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Query Match	74.4%;	Score 96;	DB 4;	Length 947;
Best Local Similarity	75.0%;	Pred. No. 5.7e-07;		

	Matches	18;	Conservative	3;	Mismatches	3;	Indels	0;	Gaps	0;
Qy	1	FRQV	DAVKLG	LPDYHKII	KQPM	24				
		:	:	:	:	:	:	:	:	:
Db	52	FRQV	DAVKI	KLPDYVTII	KQPM	75				

```

RESULT 8
US-09-418-710-42
; Sequence 42, Application US/09418710
; Patent NO. 6596482
; GENERAL INFORMATION:
; APPLICANT: Jones, Michael H.
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
; FILE REFERENCE: 06501-042001
; CURRENT APPLICATION NUMBER: US/09/418,710
; CURRENT FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: PCT/JP98/01783
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: JP 9/310027
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: JP 9/116570
; PRIOR FILING DATE: 1997-04-18
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-418-710-42

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Query Match	69.0%	Score 89;	DB 4;	Length 61;
Best Local Similarity	66.7%	Pred. No. 3.3e-07;		
Matches 16;	Conservative	2;	Mismatches 6;	Indels 0;
				Gaps 0;

Qy	1	F R Q P V D A V K L G L P D Y H K I I K Q M N D	24
		:	
		:	
Dd	4	F R Q P V D P O L L G I P D Y E D I V K N M D	27
		:	
		:	

```

RESULT 9
US-09-418-710-55
; Sequence 55, Application US/09418710
; Patent No. 6596482
; GENERAL INFORMATION:
; APPLICANT: Jones, Michael H.
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
; FILE REFERENCE: 06501-042001
; CURRENT APPLICATION NUMBER: US/09/418,710
; CURRENT FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: PCT/JP98/01783
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: JP 9/310027
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: JP 9/116570
; PRIOR FILING DATE: 1997-04-18
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-418-710-55

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Query Match	68.2%;	Score 88;	DB 4;	Length 61;
Best Local Similarity	66.7%;	Pred. No. 4.7e-07;		
Matches 16;	Conservative	2;	Mismatches 6;	Indels 0;
				Gaps 0;

QY 1 F R Q P V D A V K L G L P D Y H K I I K Q P M D 24
 | | | | | : | | |
D6 4 F R Q P V D P O L L G I P D Y F D I V K M P M D 27
 | | | | | : | | |

```
RESULT 10
US-08-227-536-2
; Sequence 2, Application US/08227536
; Patent No. 5658784
; GENERAL INFORMATION:
; APPLICANT: Eckner, Richard
; APPLICANT: Ewen, Mark
; APPLICANT: Livingston, David
; TITLE OF INVENTION: NUCLEIC ACID, ENCODING TRANSCRIPTION
; TITLE OF INVENTION: FACTOR P300 AND USES OF P300
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes
; STREET: Ten Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/227,536
; FILING DATE: 14-APR-1994
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Ph.D., Kathleen A.
; REGISTRATION NUMBER: 34,380
; REFERENCE/DOCKET NUMBER: DFCI-308XX
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-2290
; TELEFAX: (617) 451-0313
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2414 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-227-536-2

Query Match 68.2%; Score 88; DB 1; Length 2414;
Best Local Similarity 66.7%; Pred. No. 3.2e-05;
Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 FRQPDVAVKGLPDYHKIKQPM 24
Db 1075 FRQPDVQLIGIPDYFDIVKSPMD 1098

RESULT 11
US-08-194-468-2
; Sequence 2, Application PC/TUS9504682
; Patent No. 5750336
; GENERAL INFORMATION:
; APPLICANT: Montminy, Marc R.
; TITLE OF INVENTION: ASSAYS FOR THE IDENTIFICATION OF
; TITLE OF INVENTION: COMPOUNDS WHICH INHIBIT ACTIVATION OF CAMP AND MITOGEN
; TITLE OF INVENTION: RESPONSIVE GENES
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/194,468
; FILING DATE: 10-FEB-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen B.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)-546-4737
; TELEFAX: (619)-546-9392
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-194-468-2

Query Match 65.2%; Score 88; DB 1; Length 2441;
Best Local Similarity 66.7%; Pred. No. 3.3e-05;

Qy 1 FRQPDVAVKGLPDYHKIKQPM 24
Db 1075 FRQPDVQLIGIPDYFDIVKSPMD 1098

RESULT 12
US-08-194-468-2
; Sequence 2, Application US/08194468
; Patent No. 5750336
; GENERAL INFORMATION:
; APPLICANT: Montminy, Marc R.
; TITLE OF INVENTION: ASSAYS FOR THE IDENTIFICATION OF
; TITLE OF INVENTION: COMPOUNDS WHICH INHIBIT ACTIVATION OF CAMP AND MITOGEN
; TITLE OF INVENTION: RESPONSIVE GENES
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/194,468
; FILING DATE: 10-FEB-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen B.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)-546-4737
; TELEFAX: (619)-546-9392
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-194-468-2

Query Match 68.2%; Score 88; DB 5; Length 2414;
Best Local Similarity 66.7%; Pred. No. 3.2e-05;
Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 FRQPDVAVKGLPDYHKIKQPM 24
Db 1075 FRQPDVQLIGIPDYFDIVKSPMD 1098
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Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 FRQPDVAVKLGPDYHKKIQPMD 24
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Db 1112 FRQPDVQLLGIPDYFDIVKNPMD 1135

RESULT 13

US-08-961-739-2
; Sequence 2, Application US/08961739A
; Patent No. 6063583
; GENERAL INFORMATION:
; APPLICANT: Montminy, Marc R.
; TITLE OF INVENTION: Methods for Treating Diabetes Mellitus
; FILE REFERENCE: SALK1650-1
; CURRENT APPLICATION NUMBER: US/08/961,739A
; CURRENT FILING DATE: 1997-10-31
; EARLIER APPLICATION NUMBER: US 194,468
; EARLIER FILING DATE: 1994-02-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 2441
; TYPE: PRT
; ORGANISM: Mus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(2441)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-08-961-739-2

Query Match 68.2%; Score 88; DB 3; Length 2441;
Best Local Similarity 66.7%; Pred. No. 3.3e-05;
Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 FRQPDVAVKLGPDYHKKIQPMD 24
||||| :||| :|||
Db 1112 FRQPDVQLLGIPDYFDIVKNPMD 1135

RESULT 14

US-09-514-247A-8
; Sequence 8, Application US/09514247A
; Patent No. 6365361
; GENERAL INFORMATION:
; APPLICANT: TANABE SEIYAKU CO. LTD.
; APPLICANT: MIZUKAMI, Junko
; TITLE OF INVENTION: METHOD FOR IDENTIFYING OR SCREENING AGONIST AND ANTAGONIST TO PPA
; FILE REFERENCE: TANIGUCHI=6
; CURRENT APPLICATION NUMBER: US/09/514,247A
; CURRENT FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: PCT/JP98/03734
; PRIOR FILING DATE: 1998-08-24
; PRIOR APPLICATION NUMBER: JP231084/1997
; PRIOR FILING DATE: 1997-08-27
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 2441
; TYPE: PRT
; ORGANISM: mouse
US-09-514-247A-8

Query Match 68.2%; Score 88; DB 4; Length 2441;
Best Local Similarity 66.7%; Pred. No. 3.3e-05;
Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 FRQPDVAVKLGPDYHKKIQPMD 24
||||| :||| :|||
Db 1112 FRQPDVQLLGIPDYFDIVKNPMD 1135

RESULT 15

US-09-686-316-2
; Sequence 2, Application US/09686316
; Patent No. 6646115
; GENERAL INFORMATION:
; APPLICANT: Montminy, Marc R.
; TITLE OF INVENTION: Methods for Treating Diabetes Mellitus
; FILE REFERENCE: SALK1650-1
; CURRENT APPLICATION NUMBER: US/09/686,316
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US/08/961,739
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: US 194,468
; PRIOR FILING DATE: 1994-02-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 2441
; TYPE: PRT
; ORGANISM: Mus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(2441)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-686-316-2

Query Match 68.2%; Score 88; DB 4; Length 2441;
Best Local Similarity 66.7%; Pred. No. 3.3e-05;
Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 FRQPDVAVKLGPDYHKKIQPMD 24
||||| :||| :|||
Db 1112 FRQPDVQLLGIPDYFDIVKNPMD 1135

Search completed: July 27, 2004, 12:01:33
Job time : 18 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: July 27, 2004, 12:00:41 ; Search time 43 Seconds
(without alignments)
174.784 Million cell updates/sec

Title: US-09-784-553C-19_COPY_29_52
Perfect score: 129
Sequence: 1 FRQPDVAVKLGPDYHKIIKQPM 24

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Gapop 10.0 , Gapext 0.5

Searched: 1288442 seqs, 313154207 residues

Total number of hits satisfying chosen parameters: 1288442

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*
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3: /cgn2_6/ptodata/2/pubpaa/US03_NEW_PUB.pep.*
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11: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
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13: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
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16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	129	100.0	111	12	US-09-784-553C-19
2	129	100.0	111	15	US-10-209-201C-19
3	129	100.0	801	14	US-10-146-473-42
4	113	87.6	111	12	US-09-784-553C-21
5	113	87.6	111	15	US-10-209-201C-21
6	110	85.3	111	12	US-09-784-553C-20
7	110	85.3	111	15	US-10-209-201C-20
8	110	85.3	140	9	US-09-764-864-1572
9	110	85.3	235	9	US-09-764-864-1159
10	107	82.9	1390	12	US-10-092-900A-224
11	96	74.4	947	14	US-10-293-822-1
12	93	72.1	111	12	US-09-784-553C-14
13	93	72.1	111	15	US-10-209-201C-14
14	92	71.3	714	16	US-10-437-963-156944
15	92	71.3	734	16	US-10-437-963-156947

16	91	70.5	723	15	US-10-369-493-3827	Sequence 3827, Ap
17	90	69.8	346	12	US-10-425-114-64125	Sequence 64125, A
18	89	69.0	61	12	US-09-839-479-41	Sequence 41, Appl
19	89	69.0	61	12	US-10-702-148-41	Sequence 41, Appl
20	89	69.0	61	12	US-10-376-537-42	Sequence 42, Appl
21	89	69.0	610	12	US-10-424-599-198828	Sequence 198828, A
22	88	68.2	61	12	US-09-839-479-54	Sequence 54, Appl
23	88	68.2	61	12	US-10-702-148-54	Sequence 54, Appl
24	88	68.2	61	12	US-10-376-537-55	Sequence 55, Appl
25	88	68.2	112	12	US-09-784-553C-11	Sequence 11, Appl
26	88	68.2	112	12	US-09-784-553C-12	Sequence 12, Appl
27	88	68.2	112	12	US-09-784-553C-13	Sequence 13, Appl
28	88	68.2	112	15	US-10-209-201C-11	Sequence 11, Appl
29	88	68.2	112	15	US-10-209-201C-12	Sequence 12, Appl
30	88	68.2	112	15	US-10-209-201C-13	Sequence 13, Appl
31	88	68.2	2441	13	US-10-109-886-8	Sequence 8, Appl
32	88	68.2	2442	13	US-10-109-886-10	Sequence 10, Appl
33	87	67.4	113	12	US-09-784-553C-25	Sequence 25, Appl
34	87	67.4	113	15	US-10-209-201C-25	Sequence 25, Appl
35	86	66.7	113	12	US-09-784-553C-23	Sequence 23, Appl
36	86	66.7	113	15	US-10-209-201C-23	Sequence 23, Appl
37	86	66.7	343	12	US-10-425-114-38300	Sequence 38300, A
38	86	66.7	575	12	US-10-425-114-63524	Sequence 63524, A
39	85	65.9	96	12	US-10-425-114-40087	Sequence 40087, A
40	85	65.9	128	12	US-10-424-599-244688	Sequence 244688, A
41	85	65.9	656	16	US-10-437-963-154093	Sequence 154093, A
42	81	62.8	478	12	US-10-425-114-62363	Sequence 62363, A
43	81	62.8	563	16	US-10-437-963-198539	Sequence 198539, A
44	81	62.8	751	16	US-10-437-963-172901	Sequence 172901, A
45	81	62.8	791	16	US-10-437-963-172902	Sequence 172902, A

ALIGNMENTS

RESULT 1
US-09-784-553C-19
; Sequence 19, Application US/09784553C
; Publication No. US20040043378A1
; GENERAL INFORMATION:
; APPLICANT: ZHOOU, MING-MING
; TITLE OF INVENTION: METHODS OF IDENTIFYING MODULATORS OF BROMODOMAINS
; FILE REFERENCE: 2459-1-003 CIP
; CURRENT APPLICATION NUMBER: US/09/784,553C
; CURRENT FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: 09/510,314
; PRIOR FILING DATE: 2000-02-22
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 19
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-784-553C-19

Query Match 100.0%; Score 129; DB 12; Length 111;
Best Local Similarity 100.0%; Pred. No. 1.7e-12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRQPDVAVKLGPDYHKIIKQPM 24
DB 29 FRQPDVAVKLGPDYHKIIKQPM 52

RESULT 2
US-10-209-201C-19
; Sequence 19, Application US/10209201C
; Publication No. US20040009613A1
; GENERAL INFORMATION:
; APPLICANT: Verdin, Eric
; APPLICANT: Bruland, Joao
; APPLICANT: Ott, Melanie


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Query Match      85.3%; Score 110; DB 12; Length 111;
Best Local Similarity 83.3%; Pred. No. 1.7e-09;
Matches 20; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 FROPVDVAVKLGLPDYHKIIKPMD 24
Db 29 FYQPVDAIKNLDPYHKIIKNPMD 52

RESULT 7
US-10-209-201C-20
; Sequence 20, Application US/10209201C
; Publication No. US20040009613A1
; GENERAL INFORMATION:
; APPLICANT: Verdine, Eric
; APPLICANT: Bruland, Joan
; APPLICANT: Ott, Melanie
; APPLICANT: Zhou, Ming-Ming
; APPLICANT: Aggarwal, Aneel
; TITLE OF INVENTION: Methods of Identifying Modulators of Bromodomains
; FILE REFERENCE: 2459-1-003CIPDIV
; CURRENT APPLICATION NUMBER: US/10/209,201C
; CURRENT FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: 09/784,553
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 09/510,314
; PRIOR FILING DATE: 2000-02-22
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-209-201C-20

Query Match      85.3%; Score 110; DB 15; Length 111;
Best Local Similarity 83.3%; Pred. No. 1.7e-09;
Matches 20; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 FROPVDVAVKLGLPDYHKIIKPMD 24
Db 29 FYQPVDAIKNLDPYHKIIKNPMD 52

RESULT 8
US-09-764-864-1572
; Sequence 1572, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1572
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-864-1572

Query Match      85.3%; Score 110; DB 9; Length 140;
Best Local Similarity 83.3%; Pred. No. 2.3e-09;
Matches 20; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 FROPVDVAVKLGLPDYHKIIKPMD 24
Db 33 FYQPVDAIKNLDPYHKIIKNPMD 56

RESULT 9
US-09-764-864-1159
; Sequence 1159, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1159
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (129)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (215)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (221)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-864-1159

Query Match      85.3%; Score 110; DB 9; Length 235;
Best Local Similarity 83.3%; Pred. No. 4.1e-09;
Matches 20; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 FROPVDVAVKLGLPDYHKIIKPMD 24
Db 33 FYQPVDAIKNLDPYHKIIKNPMD 56

RESULT 10
US-10-092-900A-224
; Sequence 224, Application US/10092900A
; Publication No. US20040043382A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Taupier Jr., Raymond J.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Li, Li
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: Gorman, Linda
; APPLICANT: Miller, Charles E.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Patturajan, Meera
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Guo, Xiaojia Sasha
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Fernandes, Elma R.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Liu, Yi
; APPLICANT: Anderson, David W.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Catterton, Elina
; APPLICANT: Leite, Mario W.
; APPLICANT: Zhong, Haihong
; APPLICANT: Alsobrook, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
```

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; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: No. US20040043382A1e1 Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-290C
; CURRENT APPLICATION NUMBER: US/10/092,900A
; CURRENT FILING DATE: 2002-03-07
; PRIOR FILING DATE: USSN 60/274,322
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USSN 60/283,675
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: USSN 60/338,092
; PRIOR FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: USSN 60/274,281
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USSN 60/274,191
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USSN 60/325,681
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: USSN 60/304,354
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: USSN 60/279,995
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: USSN 60/294,899
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: USSN 60/287,424
; PRIOR FILING DATE: 2001-04-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 788
; SEQ ID NO 224
; LENGTH: 1390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-092-900A-224

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Query Match      82.9%; Score 107; DB 12; Length 1390;
Best Local Similarity 83.3%; Pred. No. 9.3e-08;
Matches 20; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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Qy 1 FRQPDVAVKLGPDYHKIKQPM 24
Db 83 FRQPDVAVKLNLPDYHKIKTPMD 106

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RESULT 11
US-10-293-822-1
; Sequence 1, Application US/10293822
; Publication No. US20030083470A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Michael H.
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
; FILE REFERENCE: 06501-043001
; CURRENT APPLICATION NUMBER: US/10/293,822
; CURRENT FILING DATE: 2002-11-12
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: US/09/418,780
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: JAPAN 9/116402
; PRIOR FILING DATE: 1997-04-18
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 947
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-822-1

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Query Match      74.4%; Score 96; DB 14; Length 947;
Best Local Similarity 75.0%; Pred. No. 3.3e-06;
Matches 18; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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Qy 1 FRQPDVAVKLGPDYHKIKQPM 24
Db 52 FRQPDVAVKLNLPDYHKIKTPMD 75

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RESULT 12
US-09-784-553C-14
; Sequence 14, Application US/09784553C
; Publication No. US20040043378A1
; GENERAL INFORMATION:
; APPLICANT: AGGARWAL, ANEEL
; APPLICANT: ZHOU, MING-MING
; TITLE OF INVENTION: METHODS OF IDENTIFYING MODULATORS OF BROMODOMAINS
; FILE REFERENCE: 2459-1-003 CIP
; CURRENT APPLICATION NUMBER: US/09/784,553C
; CURRENT FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: 09/510,314
; PRIOR FILING DATE: 2000-02-22
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-784-553C-14

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Query Match      72.1%; Score 93; DB 12; Length 111;
Best Local Similarity 70.8%; Pred. No. 8.5e-07;
Matches 17; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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Qy 1 FRQPDVAVKLGPDYHKIKQPM 24
Db 29 FRQPDVAKLNLPDYHKIKRPM 52

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RESULT 13
US-10-209-201C-14
; Sequence 14, Application US/10209201C
; Publication No. US20040009613A1
; GENERAL INFORMATION:
; APPLICANT: Verdin, Eric
; APPLICANT: Bruland, Joan
; APPLICANT: Ott, Melanie
; APPLICANT: Zhou, Ming-Ming
; APPLICANT: Aggarwal, Ansel
; TITLE OF INVENTION: Methods of Identifying Modulators of Bromodomains
; FILE REFERENCE: 2459-1-003CIPDIV
; CURRENT APPLICATION NUMBER: US/10/209,201C
; CURRENT FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: 09/784,553
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 09/510,314
; PRIOR FILING DATE: 2000-02-22
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-209-201C-14

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Query Match      72.1%; Score 93; DB 15; Length 111;
Best Local Similarity 70.8%; Pred. No. 8.5e-07;
Matches 17; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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Qy 1 FRQPDVAVKLGPDYHKIKQPM 24
Db 29 FRQPDVAKLNLPDYHKIKRPM 52

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RESULT 14
US-10-437-963-156944
; Sequence 156944, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.

```

```
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 156944
; LENGTH: 714
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_56563C.1.pep
US-10-437-963-156944
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Query Match          71.3%; Score 92; DB 16; Length 714;
Best Local Similarity 70.8%; Pred. No. 1e-05;
Matches 17; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 FROPDAVKLGLPDYHKIKQPM 24
Db 187 FDSFVDAVKLNIPIFYQIIKKPMD 210
```

```
RESULT 15
US-10-437-963-156947
; Sequence 156947, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 156947
; LENGTH: 734
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_56566C.1.pep
US-10-437-963-156947
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Query Match          71.3%; Score 92; DB 16; Length 734;
Best Local Similarity 70.8%; Pred. No. 1.1e-05;
Matches 17; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
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Qy 1 FROPDAVKLGLPDYHKIKQPM 24
Db 181 FDSFVDAVKLNIPIFYQIIKKPMD 204
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Search completed: July 27, 2004, 12:06:09
Job time : 44 secs
```



GenCore version 5.1.6
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CM protein - protein search, using sw model

Run on: July 27, 2004, 12:05:22 ; Search time 16 Seconds
(without alignments)
144.287 Million cell updates/sec

Title: US-09-784-553C-19_COPY_29_52
Perfect score: 129
Sequence: 1 FRQPDVAVKGLPDYHKIIKQPM 24

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	129	100.0	733	2 T28145	RING3 kinase - chicken
2	129	100.0	754	2 A56619	female sterile hom
3	113	87.6	2038	2 A43742	female sterile hom
4	97	75.2	374	2 T33328	hypothetical prote
5	93	72.1	2027	2 S60123	hypothetical prote
6	93	72.1	2056	2 G85564	protein R10E11.1 [
7	91	70.5	461	2 D96757	hypothetical prote
8	88	68.2	2414	2 A54277	transcription adap
9	88	68.2	2440	2 S39162	transcription coac
10	88	68.2	2441	2 S39161	CREB-binding prote
11	86	66.7	440	2 H86312	F2H15_2 protein -
12	86	66.7	1087	2 T22847	hypothetical prote
13	86	66.7	1250	2 T22845	hypothetical prote
14	86	66.7	3190	2 T13828	CREB-binding prote
15	83	64.3	678	2 T49984	bromodomain protei
16	78	60.5	400	2 T00472	probable RING3 pro
17	77	59.7	578	2 T40984	transcription fact
18	77	59.7	638	2 S67605	hypothetical prote
19	76	58.9	686	2 S55955	bromodomain protei
20	73	56.6	361	2 T42517	bromodomain protei
21	72	55.8	703	2 T48600	kinase-like protei
22	72	55.8	769	2 E96613	hypothetical prote
23	70	54.3	766	2 A86198	hypothetical prote
24	69	53.5	1051	2 S55259	TIF1 protein - neu
25	67	51.9	405	2 T21433	hypothetical prote
26	67	51.9	452	2 T21435	hypothetical prote
27	67	51.9	510	2 T21430	hypothetical prote
28	63	48.8	369	2 T46098	hypothetical prote
29	63	48.8	586	2 T47620	histon acetyltrans

30	61	47.3	439	1 S28051	transcription fact
31	61	47.3	454	2 T37933	transcription acti
32	60	46.5	556	2 D96791	hypothetical prote
33	58	45.0	1865	1 I48155	transcription init
34	58	45.0	1893	1 A40262	transcription init
35	57	44.2	1490	2 S32373	DNA-binding protei
36	57	44.2	2068	2 A47371	transcription init
37	55	42.6	1638	2 A42091	transcription acti
38	54	41.9	979	2 T40006	hypothetical prote
39	54	41.9	1633	2 JC5056	polypromo 1 - chic
40	53	41.1	1474	2 T20488	hypothetical prote
41	52	40.3	263	2 T09523	proliferating cell
42	52	40.3	264	2 H84697	hypothetical prote
43	52	40.3	449	2 T12495	hypothetical prote
44	52	40.3	757	2 S68142	probable transcrip
45	50	38.8	236	2 S14414	proliferating cell

ALIGNMENTS

RESULT 1

T28145
RING3 kinase - chicken
C:Species: Gallus gallus (chicken)
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000
C:Accession: T28145
R:Milne S.; Kaufman, J.; Beck, S.
submitted to the EMBL Data Library, May 1998
A:Description: DNA sequencing and analysis of the chicken major histocompatibility comp
A:Reference number: Z20475
A:Accession: T28145
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-733 <MIL>
A:Cross-references: EMBL:AL023516; NID:e1292539; PID:e1292549; PIDN:CAA18965.1
A:Experimental source: clone cH12
C:Genetics:
A:Gene: RING3
A:Map position: 16
A:Introns: 64/3; 110/3; 158/1; 227/3; 351/3; 394/3; 479/3; 546/2; 650/1; 691/1
C:Superfamily: unassigned bromodomain proteins; bromodomain homology
F:52-103/Domain: bromodomain homology <BRO1>
F:323-380/Domain: bromodomain homology <BRO2>

Query Match	100.0%	Score 129;	DB 2;	Length 733;
Best Local Similarity	100.0%;	Pred. No. 2.3e-12;		
Matches	24;	Conservative	0;	Mismatches 0;
Indels	0;	Gaps	0;	
QY	1	FRQPDVAVKGLPDYHKIIKQPM 24		
DB	52	FRQPDVAVKGLPDYHKIIKQPM 75		

RESULT 2

A56619
female sterile homeotic (fsh) homolog RING3 - human
C:Species: Homo sapiens (man)
C>Date: 21-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 20-Sep-1999
C:Accession: A56619; S18860; S40781
R:Beck, S.; Hanson, I.; Kelly, A.; Pappin, D.J.; Trowsdale, J.
DNA Seq. 2, 203-210, 1992
A>Title: A homologue of the Drosophila female sterile homeotic (fsh) gene in the class I
A:Reference number: A56619; MUID:92329974; PMID:1352711
A:Accession: A56619
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-754 <BSC>
A:Cross-references: EMBL:X62083; NID:g31471; PIDN:AAA68890.1; PID:g31472; EMBL:M80613; N
A>Note: sequence extracted from NCBI Backbone (NCBIF:108781)
C:Genetics:
A:Gene: RING3
C:Superfamily: unassigned bromodomain proteins; bromodomain homology

C;Keywords: duplication
 F;52-109/Domain: bromodomain homology <BRO1>
 F;325-382/Domain: bromodomain homology <BRO2>

Query Match 100.0%; Score 129; DB 2; Length 754;
 Best Local Similarity 100.0%; Pred. No. 2.4e-12;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRQPVDAVKLGDPDYHKIKQPM 24
 ||||| ||||| ||||| ||||| |||||
 Db 52 FRQPVDAVKLGDPDYHKIKQPM 75

RESULT 3

A43742 female sterile homeotic protein, 205K - fruit fly (Drosophila melanogaster)
 N;Alternate names: membrane protein fish, 205K
 N;Contains: female sterile homeotic protein, 110K
 C;Species: Drosophila melanogaster
 C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 20-Sep-1999
 C;Accession: A43742; B43742
 R;Haynes, S.R.; Mozer, B.A.; Bhatia-Dey, N.; Dawid, I.B.
 Dev. Biol. 134, 246-257, 1989
 A;Title: The Drosophila fish locus, a maternal effect homeotic gene, encodes apparent mem
 A;Reference number: A43742; MUID:89276730; PMID:2567251
 A;Accession: A43742
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-2038 <HAY>
 A;Cross-references: EMBL:M23221; NID:g157452; PIDN:AAA28540.1; PID:g157453
 A;Accession: B43742
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-1106 <HA2>
 A;Cross-references: EMBL:M23222
 C;Genetics:
 A;Gene: fish
 A;Cross-references: FlyBase:FBgn004656
 C;Superfamily: unassigned bromodomain proteins; bromodomain homology
 C;Keywords: alternative splicing; transmembrane protein
 F;1-2038/Product: female sterile homeotic protein, 205K #status predicted <HA2>
 F;1-1106/Product: female sterile homeotic protein, 110K #status predicted <HA2>
 F;59-116/Domain: bromodomain homology <BRO1>
 F;503-560/Domain: bromodomain homology <BRO2>

Query Match 87.5%; Score 113; DB 2; Length 2038;
 Best Local Similarity 87.5%; Pred. No. 2.9e-09;
 Matches 21; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FRQPVDAVKLGDPDYHKIKQPM 24
 ||||| ||||| ||||| ||||| |||||
 Db 59 FQQPVDAKLNLPDYHKIKQPM 82

RESULT 4

T33328 hypothetical protein F13C5.2 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 02-Sep-2000
 C;Accession: T33328
 R;Wohlmann, P.; Hawkins, J.; Gillam, B.
 Submitted to the EMBL Data Library, July 1998
 A;Description: The sequence of C. elegans cosmid F13C5.
 A;Reference number: Z21324
 A;Accession: T33328
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-374 <WOH>
 A;Cross-references: EMBL:AF077531; PIDN:AAC64610.1; GSPDB:GN00028; CESP:F13C5.2
 A;Experimental source: strain Bristol N2; clone F13C5
 C;Genetics:
 A;Gene: CESP:F13C5.2
 A;Map position: X

A;introns: 25/3; 135/3; 189/3; 313/1
 C;Superfamily: bromodomain homology
 F;141-198/Domain: bromodomain homology <BRO>

Query Match 75.2%; Score 97; DB 2; Length 374;
 Best Local Similarity 70.8%; Pred. No. 1.4e-07;
 Matches 17; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 FRQPVDAVKLGDPDYHKIKQPM 24
 ||||| ||||| ||||| ||||| |||||
 Db 141 FRQPVVVLLGLTDYHEVIKQPM 164

RESULT 5

S60123 hypothetical protein R10E11.1 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 02-Aug-2002
 C;Accession: S60123; S40713
 R;Ainscough, R.; Mortimore, B.
 Submitted to the EMBL Data Library, November 1995
 A;Reference number: S60123
 A;Accession: S60123
 A;Molecule type: DNA
 A;Residues: 1-2027 <AIN>
 A;Cross-references: EMBL:Z29095; NID:g436453; PID:g1067032
 A;Note: this is a revision to the sequence from reference S40713
 R;Ainscough, R.; Mortimore, B.
 Submitted to the EMBL Data Library, December 1993
 A;Reference number: S40713
 A;Accession: S40713
 A;Molecule type: DNA
 A;Residues: 1-466, 'CKYITRRVASFSLGK', 467, 'PEHFR', 474-475, 'KRLFPKSLHSHF', 479-1986, 'GQ'
 A;Cross-references: EMBL:Z29095
 A;Note: this sequence has been revised in reference S60123
 C;Genetics:
 A;introns: 14/1; 39/3; 302/3; 424/3; 467/1; 517/1; 688/1; 1759/1; 1828/2; 1892/3; 1964/3
 C;Superfamily: transcription coactivator CREB-binding protein; bromodomain homology
 F;889-946/Domain: bromodomain homology <BRO>

Query Match 72.1%; Score 93; DB 2; Length 2027;
 Best Local Similarity 70.8%; Pred. No. 4.6e-06;
 Matches 17; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 FRQPVDAVKLGDPDYHKIKQPM 24
 ||||| ||||| ||||| ||||| |||||
 Db 889 FRQPVDAKLNLPDYHEIKQPM 912

RESULT 6

G88564 protein R10E11.1 [imported] - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 02-Aug-2002
 C;Accession: G88564
 R;anonymus, The C. elegans Sequencing Consortium.
 Science 282, 2012-2018, 1998
 A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
 A;Reference number: A75000; MUID:99069613; PMID:9851916
 A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_eleg
 A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
 A;Accession: G88564
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-2056 <STO>
 A;Cross-references: GB:chr_III; PIDN:CAA82353.1; PID:g3979836; GSPDB:GN00021; CESP:R10E11
 C;Genetics:
 A;Gene: R10E11.1
 A;Map position: 3
 C;Superfamily: transcription coactivator CREB-binding protein; bromodomain homology
 Query Match 72.1%; Score 93; DB 2; Length 2056;
 Best Local Similarity 70.8%; Pred. No. 4.7e-06;

Matches 17; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 FRQPVDAVKGGLPDYHKIIKQPM 24
 Db 889 FRVFDVAKULNPDIYHEIIKRPMD 912

RESULT 7
 D96757
 hypothetical protein T18K17.19 [imported] - Arabidopsis thaliana
 C/Species: Arabidopsis thaliana (mouse-ear cress)
 C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 C/Accession: D96757
 R/Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Mailfi, R.; Marziali,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A/Reference number: A86141; MUID:21016719; PMID:11130712
 A/Accession: D96757
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-461 <STO>
 A/Cross-references: GB:AE005173; NID:g6598866; PIDN:AAF18720.1; GSPDB:GN00141
 C/Genetics:
 A/Gene: T18K17.19
 A/Map position: 1

Query Match 70.5%; Score 91; DB 2; Length 461;
 Best Local Similarity 70.8%; Pred. No. 1.7e-06;
 Matches 17; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 FRQPVDAVKGGLPDYHKIIKQPM 24
 Db 139 FNTFVDVTLGLHDYHNIKRPMD 162

RESULT 8
 A54277
 transcription adaptor protein p300 - human
 C/Species: Homo sapiens (man)
 C/Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 02-Aug-2002
 C/Accession: A54277; S60344
 R/Eckner, R.; Ewen, M.E.; Newsome, D.; Gerdes, M.; DeCaprio, J.A.; Lawrence, J.B.; Livin
 Genes Dev. 8, 869-884, 1994
 A/Title: Molecular cloning and functional analysis of the adenovirus E1A-associated 300-
 A/Reference number: A54277; MUID:95011587; PMID:7523245
 A/Accession: A54277
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-2414 <ECK>
 A/Cross-references: GB:U01877; NID:g495300; PIDN:AAA18639.1; PID:g495301
 A/Note: in the authors' translation '941-Ser is shown after 961 and consequently, residue
 R/Lundblad, J.R.; Kwok, R.P.S.; Laurance, M.E.; Harter, M.L.; Goodman, R.H.
 Nature 374, 85-88, 1995
 A/Title: Adenoviral E1A-associated protein p300 as a functional homologue of the transcr
 A/Reference number: S60344; MUID:95174889; PMID:7870179
 A/Accession: S60344
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 552-660 <LUN>
 C/Genetics:
 A/Gene: GDB:EF300
 A/Cross-references: GDB:9862958; OMIM:502700
 A/Map position: 22q13.2-22q13.2
 C/Superfamily: transcription coactivator CREB-binding protein; bromodomain homology
 C/Keywords: phosphoprotein; transcription; zinc finger
 F:1075-1132/Domain: bromodomain homology <BRO>

F:89.507,1136,1295,1497,1834,1977,2062,2320/Binding site: phosphate (Ser) (covalent) (by
 F:1734/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted

Query Match 68.2%; Score 88; DB 2; Length 2414;
 Best Local Similarity 66.7%; Pred. No. 3.6e-05;
 Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 FRQPVDAVKGGLPDYHKIIKQPM 24
 Db 1075 FRQPVDPQLGIPDYFDIVKSPMD 1098

RESULT 9
 S39162
 transcription coactivator CREB-binding protein - human
 N/Alternate names: CBP; RSTS; Rubinstein-Taybi syndrome (RTS) protein
 C/Species: Homo sapiens (man)
 C/Date: 07-Oct-1994 #sequence_revision 17-Nov-1995 #text_change 02-Aug-2002
 C/Accession: S39162; S60345; I58096
 R/Chrivia, J.C.; Kwok, R.P.S.; Lamb, N.; Hagiwara, M.; Montminy, M.R.; Goodman, R.H.
 Nature 365, 855-859, 1993
 A/Title: Phosphorylated CREB binds specifically to the nuclear protein CBP.
 A/Reference number: S39161; MUID:94019866; PMID:8413673
 A/Accession: S39162
 A/Molecule type: mRNA
 A/Residues: 1-2440 <CHR>
 A/Note: differences with the mouse sequence are shown
 R/Lundblad, J.R.; Kwok, R.P.S.; Laurance, M.E.; Harter, M.L.; Goodman, R.H.
 Nature 374, 85-88, 1995
 A/Title: Adenoviral E1A-associated protein p300 as a functional homologue of the transcr
 A/Reference number: S60344; MUID:95174889; PMID:7870179
 A/Accession: S60345
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 'S', 574-670, 'T', 672-681 <LUN>
 R/Petri, F.; Giles, R.H.; Dauwerse, H.G.; Saris, J.J.; Hennekam, R.C.; Maasuno, M.; Tom
 Nature 376, 348-351, 1995
 A/Title: Rubinstein-Taybi syndrome caused by mutations in the transcriptional co-activ
 A/Reference number: I58096; MUID:95356817; PMID:7630403
 A/Accession: I58096
 A/Status: translation not shown; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 352-356 <PET>
 A/Cross-references: GB:U89354; NID:gi1888537; GB:S78936; NID:gl041931
 A/Note: This translation is not annotated in GenBank entry S78936, release 112.0
 A/Note: This sequence with a termination mutation is from a patient with Rubinstein-Tay
 C/Genetics:
 A/Gene: GDB:CREBBP; RTS; CBP; RSTS
 A/Cross-references: GDB:437159; OMIM:180849; OMIM:600140
 A/Map position: 16p13.3-16p13.3
 A/Note: defects in this gene may result in Rubinstein-Taybi syndrome
 C/Superfamily: transcription coactivator CREB-binding protein; bromodomain homology
 C/Keywords: phosphoprotein; transcription; zinc finger
 F:462-661/Domain: CREB binding #status predicted <CBB>
 F:1111-1168/Domain: bromodomain homology <BRO>
 F:1283-1311/Region: zinc finger CCCC motif
 F:1707-1732/Region: zinc finger CCCC motif
 F:78.381,745,1172,1533,2063,2354/Binding site: phosphate (Ser) (covalent) (by calmodulin
 F:1771/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted

Query Match 68.2%; Score 88; DB 2; Length 2440;
 Best Local Similarity 66.7%; Pred. No. 3.6e-05;
 Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 FRQPVDAVKGGLPDYHKIIKQPM 24
 Db 1111 FRQPVDPQLGIPDYFDIVKSPMD 1134

RESULT 10
 S39161
 CREB-binding protein - mouse
 C/Species: Mus musculus (house mouse)

C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 02-Aug-2002
 C;Accession: S39161
 R;Christia, J.C.; Kwok, R.P.S.; Lamb, N.; Hagiwara, M.; Montminy, M.R.; Goodman, R.H.
 Nature 365, 855-859, 1993
 A;Title: Phosphorylated CREB binds specifically to the nuclear protein CBP.
 A;Reference number: S39161; MUID:94019866; PMID:8413673
 A;Accession: S39161
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-2441 <CHR>
 A;Cross-references: GB:S66385; NID:9435854; PIDN:AAB28651.1; PID:9435855
 C;Superfamily: transcription coactivator CREB-binding protein; bromodomain homology
 F;1112-1169/Domain: bromodomain homology <BRO>

Query Match 58.2%; Score 88; DB 2; Length 2441;
 Best Local Similarity 66.7%; Pred. No. 3.6e-05;
 Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 FRQPVDAVKLGPDYHKIKQPM 24
 ||||| ||||| ||||| ||||| |||||
 Db 1112 FRQPVDAVKLGPDYHKIKQPM 1135

RESULT 11
 H86312
 F2H15.2 protein - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Nov-2001
 C;Accession: H86312
 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Pederspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A;Reference number: H86141; MUID:21016719; PMID:11130712
 A;Accession: H86312
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-440 <STO>
 A;Cross-references: GB:AE005172; NID:g9665057; PIDN:AAF97259.1; GSPDB:GN00141
 A;Map position: 1

Query Match 66.7%; Score 86; DB 2; Length 440;
 Best Local Similarity 66.7%; Pred. No. 1e-05;
 Matches 15; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 FRQPVDAVKLGPDYHKIKQPM 24
 ||||| ||||| ||||| ||||| |||||
 Db 152 FNVPVDAKGLGPDYHKIKQPM 175

RESULT 12
 T22847
 hypothetical protein F57C7.1b - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000
 C;Accession: T22847
 R;White, S.
 Submitted to the EMBL Data Library, February 1996
 A;Reference number: Z19625
 A;Accession: T22847
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-1087 <WIL>
 A;Cross-references: EMBL:Z69646; PIDN:CAA93475.1; GSPDB:GN00028; CESP:F57C7.1b
 A;Experimental source: clone F57C7
 C;Genetics:

A;Gene: CESP:F57C7.1b
 A;Map position: X
 A;Introns: 262/3; 351/3; 391/3; 627/3; 795/2; 957/1
 C;Superfamily: bromodomain homology
 F;307-364/Domain: bromodomain homology <BRO1>
 F;579-636/Domain: bromodomain homology <BRO2>

Query Match 66.7%; Score 86; DB 2; Length 1087;
 Best Local Similarity 58.3%; Pred. No. 2.9e-05;
 Matches 14; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 FRQPVDAVKLGPDYHKIKQPM 24
 ||||| ||||| ||||| ||||| |||||
 Db 307 FQLEPDAKLEIPEYHNIVNTPMD 330

RESULT 13
 T22845
 hypothetical protein F57C7.1a - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000
 C;Accession: T22845
 R;White, S.
 Submitted to the EMBL Data Library, February 1996
 A;Reference number: Z19625
 A;Accession: T22845
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-1250 <WIL>
 A;Cross-references: EMBL:Z69646; PIDN:CAA93473.1; GSPDB:GN00028; CESP:F57C7.1a
 A;Experimental source: clone F57C7
 C;Genetics:

A;Gene: CESP:F57C7.1a
 A;Map position: X
 A;Introns: 262/3; 351/3; 391/3; 431/3; 667/3; 835/2; 997/1; 1127/1; 1218/3
 C;Superfamily: bromodomain homology
 F;307-364/Domain: bromodomain homology <BRO1>
 F;619-676/Domain: bromodomain homology <BRO2>

Query Match 66.7%; Score 86; DB 2; Length 1250;
 Best Local Similarity 58.3%; Pred. No. 3.5e-05;
 Matches 14; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 FRQPVDAVKLGPDYHKIKQPM 24
 ||||| ||||| ||||| ||||| |||||
 Db 307 FQLEPDAKLEIPEYHNIVNTPMD 330

RESULT 14
 T13828
 CREB-binding protein homolog - fruit fly (Drosophila melanogaster)
 C;Species: Drosophila melanogaster
 C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Nov-2000
 C;Accession: T13828
 R;Akimaru, H.; Chen, Y.; Dai, P.; Hou, D.X.; Nonaka, M.; Smolik, S.M.; Armstrong, S.; Go
 Nature 386, 735-738, 1997
 A;Title: Drosophila CBP is a co-activator of cubitus interruptus in hedgehog signalling.
 A;Reference number: Z17785; MUID:97263578; PMID:9109493
 A;Accession: T13828
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-3190 <AKI>
 A;Cross-references: EMBL:U88570; NID:g1916929; PID:g1916930; PIDN:AAB53050.1
 C;Genetics:
 A;Cross-references: FlyBase:FBgn0015624
 A;Map position: X
 C;Superfamily: bromodomain homology
 F;1723-1780/Domain: bromodomain homology <BRO>

Query Match 66.7%; Score 86; DB 2; Length 3190;
 Best Local Similarity 62.5%; Pred. No. 0.0001;
 Matches 15; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 FROPVDAVKLGDPDYHKIKQPM 24
||| ||| ||| :||| :||| :|||
Db 1723 FRYPVDPQALGIDYFEIVKPKND 1746

RESULT 15
T49984
bromodomain protein-like - Arabidopsis thaliana
N;Alternate names: protein F12B17.100
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Sep-2000
C;Accession: T49984
R;Bevan, M.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.
submitted to the Protein Sequence Database, April 2000
A;Reference number: Z25026
A;Accession: T49984
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-678 <BEV>
A;Cross-references: EMBL:AL353995; GSPDB:GN00063; ATSP:F12B17.100
A;Experimental source: cultivar Columbia; BAC clone F12B17
C;Genetics:
A;Gene: ATSP:F12B17.100
A;Map position: 5
A;Introns: 73/3; 560/3; 629/1; 656/2
C;Superfamily: bromodomain homology
F;269-326/Domain: bromodomain homology <BRO>

Query Match 64.3%; Score 83; DB 2; Length 678;
Best Local Similarity 62.5%; Pred. No. 5,1e-05;
Matches 15; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 FROPVDAVKLGDPDYHKIKQPM 24
||| ||| ||| :||| :||| :|||
Db 269 FLNPDVAVGLGLHDYHRIVDKPM 292

Search completed: July 27, 2004, 12:08:51
Job time : 17 secs

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OM protein - protein search, using sw model

Run on: July 27, 2004, 12:01:36 ; Search time 14 Seconds
(without alignments)
89.263 Million cell updates/sec

Title: US-09-784-553C-19_COPY_29_52
Perfect score: 129
Sequence: 1 FRQPVDAVKLGLPDYHKIKQPM D 24

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	129	100.0	801	1 BRD2 HUMAN	P25440 homo sapien
2	113	87.6	2038	1 FSH DROME	P13709 drosophila
3	110	85.3	726	1 BRD3 HUMAN	Q15059 homo sapien
4	107	82.9	1362	1 BRD4 HUMAN	Q60885 homo sapien
5	93	72.1	2056	1 CBP1 CAEL	P34545 caenorhabdi
6	88	68.2	2414	1 P300 HUMAN	Q09472 homo sapien
7	88	68.2	2441	1 CBP MOUSE	P45481 mus musculus
8	88	68.2	2442	1 CBP HUMAN	Q92793 homo sapien
9	79	61.2	727	1 YK82 SCHPO	Q9hgdp4 schizosacch
10	76	58.9	686	1 BDF1 YEAST	P35817 saccharomyc
11	69	53.5	1050	1 TFLA HUMAN	O15164 homo sapien
12	69	53.5	1051	1 TFLA MOUSE	Q64127 mus musculus
13	68	52.7	2269	1 WDR3 HUMAN	Q9ns16 homo sapien
14	67.5	52.3	1127	1 TFIIG HUMAN	Q9upn9 homo sapien
15	61	47.3	439	1 GCN5 YEAST	Q03330 saccharomyc
16	58	45.0	1872	1 T2D1 HUMAN	P21675 homo sapien
17	57	44.2	2065	1 T2D1 DROME	P51123 drosophila
18	55	42.6	1484	1 CES2 HUMAN	Q9bxf3 homo sapien
19	55	42.6	1638	1 BRM DROME	P25439 drosophila
20	52	40.3	263	1 PCN1 ARATH	Q9mrg7 arabidopsis
21	52	40.3	263	1 PCNA BRANA	Q34124 brassica na
22	52	40.3	264	1 PCN2 ARATH	Q9zw35 arabidopsis
23	52	40.3	1972	1 BA2B HUMAN	Q9uif8 homo sapien
24	52	40.3	2130	1 BA2B CHICK	Q9del13 gallus gall
25	50	38.8	236	1 PCNA SOYBN	P22177 glycine max
26	50	38.8	264	1 PCNA POPNI	Q9may3 populus nig
27	49	38.0	739	1 PURL LISIN	Q92an9 listeria in
28	49	38.0	739	1 PURL LISMO	Q8ygc1 listeria mo
29	49	38.0	830	1 GCL2 MOUSE	Q9jhd2 mus musculus
30	49	38.0	837	1 GCL2 HUMAN	Q92830 homo sapien
31	49	38.0	1058	1 BRD1 HUMAN	Q95696 homo sapien
32	49	38.0	1556	1 BAI1 HUMAN	Q9nrl2 h bromodoma
33	48.5	37.6	199	1 YECD_ECOLI	P37347 escherichia

ALIGNMENTS

RESULT 1

ID	BRD2 HUMAN	STANDARD;	PRT;	801 AA.
AC	P25440; Q00699; Q00700; Q15310; Q969U4;			
DT	01-MAY-1992 (Rel. 22, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Bromodomain-containing protein 2 (RING3 protein) (O27.1.1.1).			
GN	BRD2 OR RING3 OR KIAA9001.			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]_TaxID=9606;			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=R-cell;			
RX	MEDLINE=92329974; PubMed=1352711;			
RA	Beck S., Hanson I., Kelly A., Pappin D.J.C., Tröwsdale J.,			
RT	"A homologue of the Drosophila female sterile homeotic (fsh) gene in			
RT	the class II region of the human MHC."			
RL	DNA Seq. 2:203-210(1992).			
RN	[2]			
RP	REVISIONS TO N-TERMINUS.			
RX	MEDLINE=96376536; PubMed=8781126;			
RA	Thorpe K.L., Abdulla S., Kaufman J., Trowsdale J., Beck S.;			
RT	"Phylogeny and structure of the RING3 gene."			
RL	Immunogenetics 44:391-396(1996).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Bone marrow;			
RA	Nomura N., Miyajima N., Sazuka T., Tanaka A., Kawarabayashi Y.,			
RA	Sato S., Nagase T., Seki T., Ishikawa K.-I., Tabata S.;			
RL	Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RA	Thorpe K.;			
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
CC	-!- SUBCELLULAR LOCATION: Nuclear (Potential).			
CC	-!- SIMILARITY: Contains 2 bromodomains.			
CC	-!- SIMILARITY: Contains 1 ET domain.			
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CC	-----			
CC	EMBL; X62083; CAA43996.1; -			
DR	EMBL; M80613; AAA68890.1; ALT_INIT.			
DR	EMBL; D42040; BAA07641.1; -			
DR	EMBL; Z84497; CAC69991.1; -			
DR	EMBL; Z96104; CAC69989.1; -			
DR	EMBL; X96670; CAA65450.1; -			
DR	HSSP; Q92831; 1B91.			


```

CC -!- ALTERNATIVE PRODUCTS;
CC Event=Alternative splicing; Named isoforms=2;
CC Name=b;
CC IsoId=P34545-1; Sequence=Displayed;
CC Name=a;
CC IsoId=P34545-2; Sequence=VSP_000557;
CC Note=No experimental confirmation available;
CC -!- SIMILARITY: Contains 1 bromodomain.
CC -!- SIMILARITY: Contains 1 ZF-type zinc finger.
CC -!- SIMILARITY: Contains 2 TAZ-type zinc fingers.
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CC -----
CC EMBL; Z29095; CAA82353.2; -
CC EMBL; Z29095; CAD18875.1; -
CC PIR; G88564; G88564.
CC WormPep; R10E11.1a; CE28069.
CC WormPep; R10E11.1b; CE21117.
CC InterPro; IPR001487; Bromodomain.
CC InterPro; IPR003101; KIX.
CC InterPro; IPR00197; TAZ_finger.
CC InterPro; IPR001965; Znf_PHD.
CC InterPro; IPR00433; Znf_ZZ.
CC Pfam; PF00439; bromodomain; 1.
CC Pfam; PF02172; KIX; 1.
CC Pfam; PF02135; zf-TAZ; 2.
CC Pfam; PF00569; ZZ; 1.
CC PRINTS; PR00503; BROMODOMAIN.
CC SMART; SM00297; BROMO; 1.
CC SMART; SM00551; Znf_TAZ; 2.
CC SMART; SM00291; Znf_ZZ; 1.
CC PROSITE; PS00633; BROMODOMAIN_1; 1.
CC PROSITE; PS00014; BROMODOMAIN_2; 1.
CC PROSITE; PS01359; ZF_PHD_1; 1.
CC PROSITE; PS01359; ZF_PHD_2; 1.
CC PROSITE; PS01359; ZF_TAZ; 2.
CC PROSITE; PS01357; ZF_ZZ_1; 1.
CC PROSITE; PS01357; ZF_ZZ_2; 1.
CC PROSITE; PS01357; ZF_ZZ_3; 1.
CC Bromodomain; Metal-binding; Zinc; Zinc-finger; Alternative splicing;
KW Repeat.
FT ZN_FING 399 505 TAZ-TYPE 1.
FT DOMAIN 881 953 BROMODOMAIN.
FT ZN_FING 1493 1534 ZZ-TYPE.
FT ZN_FING 1550 1631 TAZ-TYPE 2.
FT DOMAIN 1687 2008 GLY/GLN-RICH.
FT VARSPLIC 467 478 SDPTQTKKQSV -> F (in isoform a).
FT FTID=VSP_000557.
SQ SEQUENCE 2056 AA; 227179 MW; 949FF4608C634F01 CRC64;
Query Match 72.1%; Score 93; DB 1; Length 2056;
Best Local Similarity 70.8%; Pred. No. 2e-06;
Matches 17; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
Qy 1 PRFPVDAKVLGLPDYHKKIQKPD 24
Db 889 FRFVDAKLNIPDYHEIKRPND 912
RESULT 6
P300 HUMAN
ID_P300 HUMAN STANDARD; PRT; 2414 AA.
AC Q09472;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE EIA-associated protein p300 (EC 2.3.1.48).
GN EP300 OR P300
OS Homo sapiens (Human).

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_taxID=9606;
 [1]
 SEQUENCE FROM N.A.
 RX MEDLINE=95011587; PubMed=7523245;
 RA Eckner R., Ewen M.E., Newsome D., Gerdes M., Decaprio J.A.,
 Lawrence J.B., Livingston D.M.;
 RT "Molecular cloning and functional analysis of the adenovirus E1A-
 associated 300-kD protein (p300) reveals a protein with properties of
 a transcriptional adaptor.";
 RL Genes Dev. 8:869-884(1994).
 [2]
 ENZYMATIC ACTIVITY.
 RX MEDLINE=97100994; PubMed=8945521;
 RA Ogryzko V.V., Schiltz R.L., Russanova V., Howard B.H., Nakatani Y.;
 RT "The transcriptional coactivators p300 and CBP are histone
 acetyltransferases.";
 RL Cell 87:953-959(1996).
 [3]
 INTERACTION WITH PCAF.
 RX MEDLINE=96300317; PubMed=8684459;
 RA Yang X.-J., Ogryzko V.V., Nishikawa J.-I., Howard B.H., Nakatani Y.;
 RT "A p300/CBP-associated factor that competes with the adenoviral
 oncoprotein E1A.";
 RL Nature 382:319-324(1996).
 [4]
 INTERACTION WITH HIF1A AND CREBBP.
 RX MEDLINE=97075102; PubMed=8917528;
 RA Arany Z., Huang L.E., Eckner R., Bhattacharya S., Jiang C.,
 Goldberg M.A., Bunn H.F., Livingston D.M.;
 RT "An essential role for p300/CBP in the cellular response to hypoxia.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:12969-12973(1996).
 [5]
 INTERACTIONS WITH NR3C1.
 RX MEDLINE=98250578; PubMed=9590696;
 RA Fryer C.J., Archer T.K.;
 RT "Chromatin remodelling by the glucocorticoid receptor requires the
 BRG1 complex.";
 RL Nature 393:88-91(1998).
 [6]
 INTERACTION WITH NCOA6.
 RX MEDLINE=20283976; PubMed=10823961;
 RA Ko L., Cardona G.R., Chin W.W.;
 RT "Thyroid hormone receptor-binding protein, an LXXLL motif-containing
 protein, functions as a general coactivator.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:6212-6217(2000).
 [7]
 INTERACTION WITH DTX1.
 RX MEDLINE=21576166; PubMed=11564735;
 RA Yamamoto N., Yamamoto S.-I., Inagaki F., Kawauchi M., Fukamizu A.,
 Kishi N., Matsuno K., Nakamura K., Weinmaster G., Okano H.,
 Nakafuku M.;
 RT "Role of Deltex-1 as a transcriptional regulator downstream of the
 Notch receptor.";
 RL J. Biol. Chem. 276:45031-45040(2001).
 [8]
 PHOSPHORYLATION, AND INTERACTION WITH TCF7L2 AND LEF1.
 RX MEDLINE=22450614; PubMed=12446687;
 RA Hecht A., Stemmler M.P.;
 RT "Identification of a promoter-specific transcriptional activation
 domain at the C-terminus of the Wnt-effector protein TCF4.";
 RL J. Biol. Chem. 278:3776-3785(2003).
 [9]
 VARIANTS BREAST CANCER PRO-827 AND GLY-1013, VARIANT PANCREATIC CANCER
 TYR-1650, AND VARIANT COLORECTAL CANCER GLN-2221.
 RX MEDLINE=20164332; PubMed=10700188;
 RA Gayther S.A., Batley S.J., Linger L., Bannister A., Thorpe K.,
 Chin S.-F., Daigo Y., Russell P., Wilson A., Sower H.M.,
 Delhanty J.D.A., Ponder B.A.J., Kouzarides T., Caldas C.;
 RT "Mutations truncating the EP300 acetylase in human cancers.";
 RL Nat. Genet. 24:300-303(2000).
 [10]

RP STRUCTURE BY NMR OF 302-418 IN COMPLEX WITH 786-826 OF HIF1A.
 RX MEDLINE=21957254; PubMed=11959990;
 RA Freedman S.Z., Sun Z.Y., Poy F., Kung A.L., Livingston D.M.,
 R Wagner G., Eck M.J.;
 RT "Structural basis for recruitment of CBP/p300 by hypoxia-inducible
 factor-1 alpha";
 RL Proc Natl Acad Sci U S A. 99:5367-5372(2002).
 CC -!- FUNCTION: Functions as histone acetyltransferase and regulates
 transcription via chromatin remodeling. Acetylates all four core
 histones in nucleosomes. Histone acetylation gives an epigenetic
 tag for transcriptional activation. Binds to and may be involved
 in the transforming capacity of the adenovirus E1A protein.
 CC -!- CATALYTIC ACTIVITY: Acetyl-CoA + histone = CoA + acetyl-histone.
 CC -!- SUBUNIT: Interacts with NR3C1, PCAF, NCOA6, LEF1 and TCF7L2. The
 TAZ-type 1 domain interacts with HIF1A. Probably part of a complex
 with HIF1A and CREBBP. Interacts with DTX1.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- PTM: Phosphorylated.
 CC -!- DISEASE: Defects in BP300 may play a role in epithelial cancer.
 CC -!- SIMILARITY: Contains 1 bromodomain.
 CC -!- SIMILARITY: Contains 2 TAZ-type zinc fingers.
 CC -!- SIMILARITY: Contains 2 TAZ-type zinc fingers.
 CC -!- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
 WWW="http://www.infobiogen.fr/services/chronocancer/Genes/P300ID97.html".
 CC -----
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 CC -----
 DR EMBL: U01877; AAA18639.1; --
 DR PIR: A54277; A54277.
 DR PDB: 1L3E; 11-FEB-03.
 DR TRASNAC: T01427; --
 DR Genew; HGNC:3373; BP300.
 DR MIM: 602700; --
 DR GO: GO:0008022; P:protein C-terminus binding; TAS.
 DR GO: GO:0003713; P:transcription co-activator activity; TAS.
 DR GO: GO:0003700; P:transcription factor activity; TAS.
 DR GO: GO:0007399; P:neurogenesis; TAS.
 DR GO: GO:0007165; P:signal transduction; TAS.
 DR InterPro: IPR001487; Bromodomain.
 DR InterPro: IPR003101; KIX.
 DR InterPro: IPR000197; TAZ finger.
 DR InterPro: IPR000433; ZnF_ZZ.
 DR Pfam: PF00439; bromodomain; 1.
 DR Pfam: PF02172; KIX; 1.
 DR Pfam: PF02135; zf-TAZ; 2.
 DR Pfam: PF00569; ZZ; 1.
 DR PRINTS: PR00503; BROMODOMAIN.
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 DR SMART: SMO0291; ZnF_ZZ; 1.
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or send an email to license@isb-sib.ch).

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DR MGD; MGI:1098280; Crebbp.
DR GO; GO:0000123; C:histone acetyltransferase complex; IDA.
DR GO; GO:0005634; C:nucleus; IDA.
DR GO; GO:0004402; F:histone acetyltransferase activity; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0003713; F:transcription co-activator activity; IDA.
DR GO; GO:0045449; P:regulation of transcription; IDA.
DR InterPro; IPR001487; Bromodomain.
DR InterPro; IPR003101; KIX.
DR InterPro; IPR000197; TAZ_finger.
DR InterPro; IPR000433; ZnF_ZZ.
DR Pfam; PF00439; bromodomain; 1.
DR Pfam; PF02172; KIX; 1.
DR Pfam; PF02135; zf-TAZ; 2.
DR Pfam; PF00589; ZZ; 1.
DR PRINTS; PR00503; BROMODOMAIN.
DR SMART; SM00297; BROMO; 1.
DR SMART; SM00551; ZnF_TAZ; 2.
DR SMART; SM00291; ZnF_ZZ; 1.
DR PROSITE; PS00633; BROMODOMAIN_1; 1.
DR PROSITE; PS50014; BROMODOMAIN_2; 1.
DR PROSITE; PS50134; ZF_TAZ; 2.
DR PROSITE; PS01357; ZF_ZZ_1; 1.
DR PROSITE; PS50135; ZF_ZZ_2; 1.
DR KX Transferase; Transcription regulation; Nuclear protein; Activator;
KW Bromodomain; Zinc-finger; Repeat; 3D-structure.
FT ZN FING 346 432
FT ZN FING 1104 1176
FT ZN FING 1702 1745
FT ZN FING 1766 1847
FT ZN FING 1062 1065
FT ZN FING 1556 1563
FT ZN FING 1944 1949
FT ZN FING 1968 1971
FT ZN FING 2082 2086
FT ZN FING 2200 2216
FT ZN FING 2296 2299
SQ SEQUENCE 2441 AA; 265474 MW; 0ABBO28C3112F419 CRC64;

Query Match 68.2%; Score 88; DB 1; Length 2441;
Best Local Similarity 66.7%; Pred. No. 1.5e-05;
Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 PRQPDVAVKLGDPYHKKIKQPD 24
D5 1112 FRQPDVQLGIPDYFDVKNPD 1135

RESULT 8
CBP_HUMAN
ID_CBP_HUMAN STANDARD; PRT; 2442 AA.
AC Q92793; Q00147; Q16376;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE CREB-binding protein (EC 2.3.1.48).
GN CREBBP OR CBP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

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```

RX MEDLINE=97385172; PubMed=9238046;
RA Sobulo O.M., Borow J., Tomek R., Reshmi S., Harden A.,
RA Schlegelberger B., Housman D., Doggett N.A., Rowley J.D.,
RA Zeleznik-Le N.J.;
RT "MLL is fused to CBP, a histone acetyltransferase, in therapy-related
RT acute myeloid leukemia with a t(11;16)(q23;p13.3).";
RL Proc. Natl. Acad. Sci. U.S.A. 94:8732-8737(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97321049; PubMed=9177780;
RA Giles R.H., Petrij F., Dauwerse H.G., den Hollander A.I.,
RA Lushnikova T., van Ommen G.J.B., Goodman R.H., Deaven L.L.,
RA Doggett N.A., Peters D.J.M., Breuning M.H.;
RT "Construction of a 1.2-Mb contig surrounding, and molecular analysis
RT of, the human CREB-binding protein (CBP/CREBBP) gene on chromosome
RT 16p13.3";
RL Genomics 42:96-144(1997).
RN [3]
RP SEQUENCE OF 1-405 FROM N.A.
RX MEDLINE=96378968; PubMed=8782817;
RA Borow J., Stanton V.P., Andresen J.M., Becher R., Behm F.G.,
RA Chaganti R.S.K., Civin C.I., Distche C., Dube I., Frischau A.M.,
RA Housman D., Mitelman P., Volinia S., Watmore A.E., Housman D.E.;
RT "The translocation t(8;16)(p11;p13) of acute myeloid leukaemia fuses
RT a putative acetyltransferase to the CREB-binding protein.";
RL Nat. Genet. 14:33-41(1996).
RN [4]
RP INTERACTION WITH PCAF.
RX MEDLINE=96300317; PubMed=8684459;
RA Yang X.-J., Ogryzko V.V., Nishikawa J.-I., Howard B.H., Nakatani Y.;
RT "A p300/CBP-associated factor that competes with the adenoviral
RT oncoprotein E1A";
RL Nature 382:319-324(1996).
RN [5]
RP INTERACTION WITH HIF1A AND EP300.
RX MEDLINE=97075102; PubMed=8917528;
RA Arany Z., Huang L.E., Eckner R., Bhattacharya S., Jiang C.,
RA Goldberg M.A., Bunn H.F., Livingston D.M.;
RT "An essential role for p300/CBP in the cellular response to hypoxia.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:12969-12973(1996).
RN [6]
RP INTERACTION WITH PML.
RX MEDLINE=99178939; PubMed=10077561;
RA Doucas V., Tini M., Egan D.A., Evans R.M.;
RT "Modulation of CREB binding protein function by the promyelocytic
RT (PML) oncoprotein suggests a role for nuclear bodies in hormone
RT signaling";
RL Proc. Natl. Acad. Sci. U.S.A. 96:2627-2632(1999).
RN [7]
RP ACETYLATION OF NCOA3.
RX MEDLINE=99418638; PubMed=10490106;
RA Chen H., Lin R.J., Xie W., Wilpitz D., Evans R.M.;
RT "Regulation of hormone-induced histone hyperacetylation and gene
RT activation via acetylation of an acetylase.";
RL Cell 98:675-686(1999).
RN [8]
RP INTERACTION WITH NCOA6.
RX MEDLINE=20325329; PubMed=10866662;
RA Mahajan M.A., Samuels H.H.;
RT "A new family of nuclear receptor coregulators that integrates nuclear
RT receptor signaling through CBP";
RL Mol. Cell. Biol. 20:5048-5063(2000).
RN [9]
RP IDENTIFICATION IN A COMPLEX WITH NCOA2; NCOA3; IKKα AND IKKβ.
RX MEDLINE=21969797; PubMed=11971985;
RA Wu R.C., Qin J., Hashimoto Y., Wong J., Xu J., Tsai S.Y., Tsai M.J.,
RA O'Malley B.W.;
RT "Regulation of SRC-3 (pCIP/ACTR/AIB-1/RAC-3/TRAM-1) coactivator
RT activity by I kappa B kinase.";
RL Mol. Cell. Biol. 22:3549-3561(2002).
RN [10]
RP STRUCTURE BY NMR OF 345-439 IN COMPLEX WITH 776-826 OF HIF1A.
RX MEDLINE=21957241; PubMed=11959977;

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Dames S.A., Martinez-Yamout M., De Guzman R.N., Dyson H.J.,
Wright P.E.;
"Structural basis for Hif-1 alpha /CBP recognition in the cellular
hypoxic response.";
Proc. Natl. Acad. Sci. U.S.A. 99:5271-5276(2002).
[11]
VARIANT RSTS PRO-1378.
MEDLINE=21231140; PubMed=11331617;
Murata T., Kurokawa R., Krones A., Tateumi K., Ishii M., Taki T.,
Masuno M., Ohashi H., Yanagisawa M., Rosenfeld M.G., Glass C.K.,
Hayashi Y.;
"Defect of histone acetyltransferase activity of the nuclear
transcriptional coactivator CBP in Rubinstein-Taybi syndrome";
Hum. Mol. Genet. 10:1071-1076(2001).
CC - FUNCTION: Acetyltransferase enzyme. Acetylates histones, giving a
specific tag for transcriptional activation. Also acetylates non-
histone proteins, like NCOA3 coactivator. Mediates cAMP-gene
regulation by binding specifically to phosphorylated CREB protein.
CC CBP, as coactivator, augments the activity of phosphorylated CREB
to activate transcription of cAMP-responsive genes.
CC - CATALYTIC ACTIVITY: Acetyl-CoA + histone = CoA + acetyl-histone.
CC - SUBUNIT: Interacts with SMAD1, SMAD2, SMAD3, PCAF and PML. The
TAZ-type 1 domain interacts with HIF1A. Found in a complex
containing NCOA2; NCOA3; IKKX; IKKB and IKK3. Interacts with
NCOA6 coactivator. Probably part of a complex with Hif1a and
BP300.
CC - SUBCELLULAR LOCATION: Nuclear.
CC - DISEASE: Involved in acute myeloid leukemias through chromosomal
translocations t(8;16)(p11;p13) involving MYST3 and CREBBP,
and t(11;16)(q23;p13.3) involving MLL/HRX and CREBBP.
CC - DISEASE: Defects in CREBBP are the cause of Rubinstein-Taybi
syndrome (RSTS) [MIM:180849]. RSTS is an autosomal dominant
disorder characterized by craniofacial abnormalities, broad
thumbs, broad big toes, mental retardation and a propensity for
development of malignancies.
CC - SIMILARITY: Contains 1 bromodomain.
CC - SIMILARITY: Contains 1 Z2-type zinc finger.
CC - SIMILARITY: Contains 2 TAZ-type zinc fingers.
CC - SIMILARITY: Contains 2 TAZ-type zinc fingers.
CC - DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
WWW="http://www.infobiogen.fr/services/chronocancer/Genes/CBPID42.html".
CC -----
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CC -----
EMBL; U47741; AAC51770.1; --
EMBL; U85962; AAC51331.1; --
EMBL; U89354; AAC51339.1; --
EMBL; U89355; AAC51340.1; --
DB; 1L8C; 24-APR-02.
DB; 1JSP; 17-AUG-02.
DR TRAF3PAC; T02214; --
Genew; HGNC:2348; CREBBP.
DR MIM; 600140; --
DR MIM; 180849; --
DR GO; GO:0005737; Cytoplasm; TAS.
DR GO; GO:0005634; Nucleus; TAS.
DR GO; GO:0004871; F:signal transducer co-activator activity; TAS.
DR GO; GO:0003713; F:transcription co-activator activity; TAS.
DR GO; GO:0003700; F:transcription factor activity; TAS.
DR GO; GO:0004611; P:protein complex assembly; TAS.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPR001487; Bromodomain.
DR InterPro; IPR003101; KIX.
DR InterPro; IPR000197; TAZ finger.
DR InterPro; IPR000433; Znf_ZZ.
Pfam; PF00439; bromodomain; 1.
Pfam; PF02172; KIX; 1.

Pfam; PF02135; zf-TAZ; 2.
Pfam; PF00569; ZZ; 1.
PRINTS; PRO0503; BROMODOMAIN.
DR SMART; SM00297; BROMO; 1.
DR SMART; SM00551; Znf_TAZ; 2.
DR SMART; SM00291; Znf_ZZ; 1.
DR PROSITE; PS00633; BROMODOMAIN_1; 1.
DR PROSITE; PS001014; BROMODOMAIN_2; 1.
DR PROSITE; PS00134; ZF_TAZ; 2.
DR PROSITE; PS00357; ZF_ZZ_1; 1.
DR PROSITE; PS00357; ZF_ZZ_2; 1.
DR PROSITE; PS00135; ZF_ZZ_1; 1.
DR PROSITE; PS00135; ZF_ZZ_2; 1.
KW Transferrase; Transcription regulation; Nuclear protein; Activator;
KW Bromodomain; Chromosomal translocation; Zinc-finger; Repeat;
KW Disease mutation; 3D-structure.
FT ZN FING 1701 1744 ZZ-TYPE.
FT ZN FING 347 433 TAZ-TYPE 1.
FT DOMAIN 452 683 CREB-BINDING.
FT DOMAIN 1103 1175 BROMODOMAIN.
FT DOMAIN 1061 1064 POLY-GLU.
FT DOMAIN 1199 1487 CYS/HIS-RICH.
FT DOMAIN 1555 1562 POLY-GLU.
FT ZN FING 1765 1846 TAZ-TYPE 2.
FT DOMAIN 1943 1948 POLY-PRO.
FT DOMAIN 1967 1970 POLY-GLN.
FT DOMAIN 2081 2085 POLY-GLN.
FT DOMAIN 2199 2216 POLY-GLN.
FT DOMAIN 2245 2248 POLY-GLN.
FT DOMAIN 2297 2300 POLY-GLN.
FT VARIANT 1378 1378 R -> P (in RSTS; abolishes
acetyltransferase activity and the
ability of transactivate CREB).
/FTID=VAR_015578.
FAE -> NSG (IN REF. 2).
ED -> VV (IN REF. 2).
V -> L (IN REF. 2).
N -> F (IN REF. 2).
T -> P (IN REF. 2).
SQ SEQUENCE 2442 AA; 285336 MW; 42D084619475F3D2 CRC64;
Query Match 68.2%; Score 88; DB 1; Length 2442;
Best Local Similarity 66.7%; Pred. No. 1.5e-05;
Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
QY 1 PRQVDVAVKLGPDYHKIKOPMD 24
DB 1111 PRQVDVAVKLGPDYHKIKOPMD 1134
RESULT 9
YK82 SCHPO
ID YK82 SCHPO STANDARD; PRT; 727 AA.
AC Q9HGF4; P78808;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical bromodomain protein C631.02.
GN SPAC631.02.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
ON NCBI_TaxID=4896;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidaigo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,

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RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Gryonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Borzpm K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Fumelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Kiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Carrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Spakevski G.V., Ussery D., Barrell B.G., Nurse P.,
RT "the genome sequence of Schizosaccharomyces pombe";
RL Nature 415:871-880(2002).
RN [2]
RP SEQUENCE OF 353-713 FROM N.A.
RC STRAIN=PR745;
RX MEDLINE=98162722; PubMed=9501991;
RA Yoshioka S., Kato K., Nakai K., Okayama H., Nojima H.;
RT "Identification of open reading frames in Schizosaccharomyces pombe
RT cDNAs.";
RL DNA Res. 4:363-369(1997).
CC -!- SIMILARITY: Contains 2 bromodomains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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DR EMBL; AL391713; CAC05484.1; -.
DR EMBL; D89157; BAA13819.1; -.
DR PIR; T42517; T42517.
DR GeneDB SPombe; SPAC631.02; -.
DR InterPro; IPR001487; Bromodomain.
DR Pfam; PF00439; bromodomain; 2.
DR PRINTS; PR00503; BROMODOMAIN.
DR SMART; SM00297; BROMO; 2.
DR PROSITE; PS00633; BROMODOMAIN 1; 1.
DR PROSITE; PS50014; BROMODOMAIN 2; 2.
DR Hypothetical protein; Bromodomain; Repeat.
FT DOMAIN 246 318 BROMODOMAIN 1.
FT DOMAIN 408 480 BROMODOMAIN 2.
SQ SEQUENCE 727 AA; 81031 MW; 5CFA73844CB6EF05 CRC64;
Query Match 61.2%; Score 79; DB 1; Length 727;
Best Local Similarity 62.5%; Pred. No. 0.00011;
Matches 15; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
QY 1 FRQPDVAVKGLPDYHKIKQPMQ 24
D5 254 FRAPDVKQNIQDYPFIKNPID 277
RESULT 10
BD1 YEAST STANDARD; PRT; 686 AA.
AC P35817; Q06048;
DT 01-JUN-1994 (Rel. 29, Created)
DT 18-JUL-1999 (Rel. 38, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE BDF1 protein.
GN BDF1 OR YLR399C OR L8084.18.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.

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OX NCBI TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=95116323; PubMed=7816623;
RA Lygerou Z., Conesa C., Lesage P., Swanson R.N., Ruet A., Carlson M.,
RA Senterac A., Seraphin B.;
RT "The yeast BDF1 gene encodes a transcription factor involved in the
RT expression of a broad class of genes including snRNAs.";
RL Nucleic Acids Res. 22:5332-5340(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA Roeder G.S., Chua P.R.;
RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RX MEDLINE=97313267; PubMed=9169871;
RA Johnston M., Hillier L., Riles L., Albermann K., Andre B., Ansorge W.,
RA Benes V., Brueckner M., Delius H., Dubois E., Duesterhoeft A.,
RA Entian K.-D., Floeth M., Goffeau A., Hebling U., Heumann K.,
RA Heuss-Neitzel D., Hilbert H., Hilger F., Kleine K., Koetter P.,
RA Louis E.J., Messenguy F., Mewes H.-W., Miosga T., Moestl D.,
RA Mueller-Auer S., Nentwich U., Obermaier B., Piravandi E., Pohl T.M.,
RA Portetelle D., Fumelle B., Rechmann S., Rieger M., Rinke M., Rose M.,
RA Scharte M., Scherens B., Scholler P., Schwager C., Schwarz S.,
RA Underwood A.P., Urrestazu L.A., Vandenbol M., Verhasselt P.,
RA Vierendeels F., Voet M., Volckaert G., Voss H., Wambutt R., Wedler E.,
RA Wedler H., Zimmermann F.K., Zollner A., Hani J., Hoheisel J.D.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XII.";
RL Nature 387:87-90(1997).
RN [4]
RP SEQUENCE OF 471-686 FROM N.A.
RX MEDLINE=93309467; PubMed=8321235;
RA Widner W.R., Wickner R.B.;
RT "Evidence that the SKI antiviral system of Saccharomyces cerevisiae
RT acts by blocking expression of viral mRNA.";
RL Mol. Cell. Biol. 13:4331-4341(1993).
CC -!- FUNCTION: Transcription factor involved in the expression of a
CC broad class of genes including snRNAs. Required for sporulation.
CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -!- SIMILARITY: Contains 2 bromodomains.
CC -!- SIMILARITY: Contains 1 ET domain.
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
DR EMBL; Z18944; CAA79377.1; -.
DR EMBL; U08116; AAB89115.1; -.
DR EMBL; U19729; AAB82357.1; -.
DR EMBL; L13469; AAA35048.1; -.
DR PIR; S55955; S55955.
DR GenOnline; 142462; -.
DR TRANSFAC; T03204; -.
DR SGD; S0004391; BDF1.
DR GO; GO:0005634; C:nucleus; IDA.
DR GO; GO:0030528; F:transcription regulator activity; IMP.
DR GO; GO:0007151; P:sporulation (sensu Saccharomycetes); IMP.
DR InterPro; IPR001487; Bromodomain.
DR Pfam; PF00439; bromodomain; 2.
DR PRINTS; PR00503; BROMODOMAIN.
DR SMART; SM00297; BROMO; 2.
DR PROSITE; PS00633; BROMODOMAIN 1; 1.
DR PROSITE; PS50014; BROMODOMAIN 2; 2.
KW Transcription regulation; Nuclear protein; Bromodomain; Repeat;
FT DOMAIN 165 237 BROMODOMAIN 1.
FT DOMAIN 332 404 BROMODOMAIN 2.

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FT DOMAIN 522 686 ET DOMAIN.
FT CONFLICT 8 8 Q -> LC (IN REF. 1).
FT CONFLICT 93 94 GA -> R (IN REF. 2).
FT CONFLICT 94 94 A -> P (IN REF. 2).
FT CONFLICT 282 282 A -> P (IN REF. 1).
FT CONFLICT 385 385 D -> E (IN REF. 1).
FT CONFLICT 493 493 A -> R (IN REF. 4).
SQ SEQUENCE 686 AA; 79978 MW; 8CCU52FA1F91D0DA CRC64;

Query Match 58.9%; Score 76; DB 1; Length 686;
Best Local Similarity 62.5%; Pred. No. 0.00033;
Matches 15; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 FRQVDVAVKLGIDYVHKIKQPMQ 24
Db 173 FLOQVDPVKLDIPFYNYIKRPMQ 196

RESULT 11
ID_TFLA_HUMAN STANDARD; PRT; 1050 AA.
AC Q15164; O95854;
DT 15-JUL-1999 (Rel. 38, Created)
DI 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Transcription intermediary factor 1-alpha (TIF1-alpha) (Tripartite
DE motif protein 24).
GN TIF1 OR TRIM24 OR TIFIA.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM SHORT).
RC TISSUE=Breast cancer;
RX MEDLINE=97277352; PubMed=9115274;
RA Thénot S., Henriquet C., Rochefort H., Cavailles V.;
RT "Differential interaction of nuclear receptors with the putative human
RT transcriptional coactivator hTIF1."
RL J. Biol. Chem. 272:12062-12068(1997).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM SHORT).
RX MEDLINE=99144725; PubMed=1002127;
RA Venturini L., You J., Stadler M., Gallien R., Lallemand V.,
RA Koken M.H.M., Mattei M.-G., Ganser A., Chambon P., Losson R.,
RA De The H.;
RT "TIF1gamma, a novel member of the transcriptional intermediary factor
RT 1 family."
RL Oncogene 18:1209-1217(1999).
RN [3]
RP SEQUENCE OF 477-510 (ISOFORM LONG).
RC TISSUE=Breast cancer;
RA Cavailles V.;
RA Submitted (JAN-1999) to Swiss-Prot.
RN [4]
RP INTERACTION WITH NR3C2.
RX MEDLINE=20388588; PubMed=10935545;
RA Hellal-Levy C., Fagart J., Souque A., Wurtz J.-M., Moras D.,
RA Rafestin-Obelin M.-E.;
RT "Crucial role of the H11-H12 loop in stabilizing the active
RT conformation of the human mineralocorticoid receptor."
RL Mol. Endocrinol. 14:1210-1221(2000).
RN [5]
RP FUNCTION: Interacts selectively in vitro with the AF2-activating
CC domain of the estrogen receptors. Association with DNA-bound
CC estrogen receptors requires the presence of estradiol.
CC -1- SUBUNIT: Interacts with CBX1 and CBX3 (By similarity). Interacts
CC with NR3C2.
CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Long;
CC IsoId=O15164-1; Sequence=Displayed;
CC Name=Short;

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CC CC IsoId=O15164-2; Sequence=VSP_005772;
CC CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
CC CC -1- SIMILARITY: Contains 2 B box-type zinc fingers.
CC CC -1- SIMILARITY: Contains 1 bromodomain.
CC CC -1- SIMILARITY: Contains 1 PHD-type zinc finger.
CC CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC CC -----
CC CC EMBL; AF009353; AAB63585.1; -.
CC CC EMBL; AF119042; AAD17258.1; -.
CC CC HSSP; P29590; 1BOR.
CC CC TRANSFAC; T04945; -.
CC CC Genew; HGNC:11812; TIF1.
CC CC MIM; 603406; -.
CC CC GO; GO:0005634; C:nucleus; TAS.
CC CC GO; GO:0005102; F:receptor binding; TAS.
CC CC GO; GO:0003713; P:transcription co-activator activity; TAS.
CC CC GO; GO:0006366; P:transcription from Pol II promoter; TAS.
CC CC InterPro; IPR003649; BBox.C.
CC CC InterPro; IPR001487; Bromodomain.
CC CC InterPro; IPR000315; Znf_Bbox.
CC CC InterPro; IPR001965; Znf_PHD.
CC CC InterPro; IPR001841; Znf_ring.
CC CC Pfam; PF00439; bromodomain; 1.
CC CC Pfam; PF00628; PHD; 1.
CC CC Pfam; PF00643; zf-B_box; 2.
CC CC Pfam; PF00097; zf-C3HC4; 1.
CC CC PRINTS; PR01406; BBOXZNFINGER.
CC CC PRINTS; PR00503; BROMODOMAIN.
CC CC SMART; SM00502; BBC; 1.
CC CC SMART; SM00336; BBOX; 2.
CC CC SMART; SM00297; BROMO; 1.
CC CC SMART; SM00249; PHD; 1.
CC CC SMART; SM00184; RING; 1.
CC CC PROSITE; PS00633; BROMODOMAIN_1; FALSE_NEG.
CC CC PROSITE; PS00014; BROMODOMAIN_2; 1.
CC CC PROSITE; PS00119; ZF_BBOX; 2.
CC CC PROSITE; PS01359; ZF_PHD_1; 1.
CC CC PROSITE; PS00016; ZF_PHD_2; 1.
CC CC PROSITE; PS00518; ZF_RING_1; 1.
CC CC PROSITE; PS00089; ZF_RING_2; 1.
CC CC Transcription regulation; Repressor; DNA-binding; Bromodomain;
KW Zinc-finger; Alternative splicing; Nuclear protein; Coiled coil;
KW Repeat.
KW DOMAIN 9 15 POLY-ALA.
FT ZN_FING 56 82 RING-TYPE.
FT ZN_FING 158 211 B_BOX-TYPE 1.
FT ZN_FING 218 259 B_BOX-TYPE 2.
FT DOMAIN 289 359 COILED COIL (POTENTIAL).
FT DOMAIN 344 347 POLY-GLN.
FT ZN_FING 754 779 NUCLEAR RECEPTOR BINDING SITE (NRBS).
FT DOMAIN 826 873 PHD-TYPE.
FT DOMAIN 891 907 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT DOMAIN 932 987 BROMODOMAIN.
FT VARSPLIC 477 510 Missing (in isoform Short).
FT CONFLICT 14 20 AASAAAS -> RLGCAP (IN REF. 1).
FT CONFLICT 24 28 SAAPS -> RGG (IN REF. 1).
FT CONFLICT 109 114 GSPVSG -> ARRSA (IN REF. 1).
FT CONFLICT 350 350 A -> T (IN REF. 1).
FT CONFLICT 600 600 D -> N (IN REF. 1).
FT CONFLICT 608 608 M -> I (IN REF. 1).
FT CONFLICT 967 967 A -> R (IN REF. 1).
SQ SEQUENCE 1050 AA; 116831 MW; D341E8022AAC67E CRC64;

Query Match 53.5%; Score 69; DB 1; Length 1050;
Best Local Similarity 68.4%; Pred. No. 0.0068;

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Query Match          53.5%;   Score 69;   DB 1;   Length 1051;
Best Local Similarity 68.4%;   Pred. No. 0.0069;
Matches 13;   Conservative 2;   Mismatches 4;   Indels 0;   Gaps 0;

QY      6  DAVKGLPDYHKIIKPMD 24
      | | | | | | | | | |
Db      927 DPVLTVPDYKIIKPMD 945

RESULT 13
WDR9_HUMAN
ID WDR9_HUMAN          STANDARD; PRT; 2269 AA.
AC Q9NSI6; O43721; OSTCV3; Q9NUK1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE WD-repeat protein 9.
GN WDR9.
OS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RA Vidal-Taboada J.M., Ramos V.C., Oliva R., Egeo A., Scartezzini P.;
RT "Identification and characterization of a novel gene in the Down
RL syndrome chromosomal region-2 from chromosome 21.";
RN Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
[2]
SEQUENCE FROM N.A.
RA MEDLINE=20289799; PubMed=10830953;
RX Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
RA Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Groner Y.,
RA Soeda E., Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K.,
RA Polley A., Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
RA Reichwald K., Rump A., Schillabel M., Schudy A., Zimmermann W.,
RA Rosenthal A., Kudon J., Shibuya K., Kawasaki K., Asakawa S.,
RA Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,
RA Minoshima S., Shimizu N., Nordieck G., Hornischer K., Brandt P.,
RA Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloecker H.,
RA Ramser J., Beck A., Klages S., Hennig S., Rieselmann L., Dagand E.,
RA Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
RA Lehrach H., Reinhardt R., Raspo M.-L.;
RT "The DNA sequence of human chromosome 21.";
RN Nature 405:311-319 (2000).
[3]
SEQUENCE OF 1586-1805 FROM N.A.
RC TISSUE=Retal heart;
RX MEDLINE=98153806; PubMed=9480850;
RA Vidal-Taboada J.M., Bergonon S., Sanchez M., Lopez-Acedo C., Groet J.,
RA Nizetic D., Egeo A., Scartezzini P., Katsanis N., Fisher E.M.C.,
RA Delabar J.M., Oliva R.;
RT "High resolution physical mapping and identification of transcribed
RN sequences in the Down syndrome region-2.";
RL Biochem. Biophys. Res. Commun. 243:572-578 (1998).
[4]
SEQUENCE OF 1868-2295 FROM N.A.
RC TISSUE=Placenta;
RX Isozaki T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA Takagatsuna M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
RA Ninomiya K., Iwayanagi T.;
RT "NEO human cDNA sequencing project.";
RN Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 8 WD repeats.
CC -!- SIMILARITY: Contains 2 bromodomains.

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RA Venturini L., You J., Stadler M., Galien R., Lallemand V.,
 RA Koken M.H.M., Mattei M.-G., Ganer A., Chambon P., Losson R.,
 RA De The H.,
 RT "TIFgamma, a novel member of the transcriptional intermediary factor
 RT 1 family.";
 RL Oncogene 18:1209-1217(1999).
 RN [2]
 RN SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
 RX MEDLINE=21231161; PubMed=11331580;
 RA Raymond A., Meroni G., Pantozzi A., Merla G., Cairo S., Luzzi L.,
 RA Risanello D., Zanaria E., Messali S., Cainarca S., Guffanti A.,
 RA Minucci S., Pelicci P.G., Ballabio A.,
 RT "The tripartite motif family identifies cell compartments.";
 RL EMBO J. 20:2140-2151(2001).
 RN [3]
 RN SEQUENCE FROM N.A. (ISOFORM ALPHA).
 RP TISSUE=Brain;
 RC MEDLINE=99397452; PubMed=10470851;
 RA Kikuno R., Nagase T., Ishikawa K.-I., Hirosewa M., Miyajima N.,
 RA Tanaka A., Kotani H., Nomura N., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. XIV.
 RT The complete sequences of 100 new cDNA clones from brain which code
 RT for large proteins in vitro.";
 RL DNA Res. 6:197-205(1999).
 RN [4]
 RN SEQUENCE OF 76-1127 FROM N.A. (ISOFORM ALPHA).
 RP TISSUE=Thyroid;
 RC MEDLINE=99367902; PubMed=10439047;
 RA Klugbauer S., Rabes H.;
 RT "The transcription coactivator ht1f and a related protein are fused
 RT to the ret receptor tyrosine kinase in childhood papillary thyroid
 RT carcinomas.";
 RL Oncogene 18:4388-4393(1999).
 CC -1- FUNCTION: Seems to act as a transcriptional repressor.
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=Alpha;
 CC IsoId=Q9UPN9-1; Sequence=Displayed;
 CC Name=Beta;
 CC IsoId=Q9UPN9-2; Sequence=VSP_005774;
 CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
 CC -1- SIMILARITY: Contains 2 B box-type zinc fingers.
 CC -1- SIMILARITY: Contains 1 bromodomain.
 CC -1- SIMILARITY: Contains 1 PHD-type zinc finger.
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 CC -----
 CC EMBL; AF119043; AAD17259.1; -
 CC EMBL; AF220136; AAG53509.1; -
 CC EMBL; AF220137; AAG53510.1; -
 CC EMBL; AB029036; BAA83065.1; ALT_INIT.
 CC EMBL; AJ132948; CAB55313.1; -
 CC TRANSFAC; T04946; -
 CC Genew; HGNC:16290; TRIM33.
 CC MIM; 605769; -
 CC GO; GO:0005634; C:nucleus; NAS.
 CC GO; GO:0003714; F:transcription co-repressor activity; ISS.
 CC GO; GO:0008270; F:zinc ion binding; NAS.
 CC GO; GO:0016481; P:negative regulation of transcription; NAS.
 CC InterPro; IPR003649; Bbox_C.
 CC InterPro; IPR001487; Bromodomain.
 CC InterPro; IPR000315; Znf_Bbox.
 CC InterPro; IPR001965; Znf_PHD.
 CC InterPro; IPR001841; Znf_RING.
 CC Pfam; PF00439; bromodomain; 1.
 CC Pfam; PF00628; PHD; 1.

DR Pfam; PF00643; zf-B_box; 2.
 DR PRINTS; PRO1406; BBOXZNFINGER.
 DR PRINTS; PRO0503; BROMODOMAIN.
 DR SMART; SM00502; BBC; 1.
 DR SMART; SM00336; BBOX; 2.
 DR SMART; SM00297; BROMO; 1.
 DR SMART; SM00249; PHD; 2.
 DR SMART; SM00184; RING; 2.
 DR PROSITE; PS00633; BROMODOMAIN_1; FALSE_NEG.
 DR PROSITE; PS00119; ZF_BBOX; 2; 1.
 DR PROSITE; PS00119; ZF_BBOX; 2; 1.
 DR PROSITE; PS01359; ZF_PHD_1; 1.
 DR PROSITE; PS00016; ZF_PHD_2; 1.
 DR PROSITE; PS00518; ZF_RING_1; 1.
 DR PROSITE; PS00089; ZF_RING_2; 1.
 KW Transcription regulation; Repressor; DNA-binding; Bromodomain;
 KW Zinc-finger; Nuclear protein; Repeat; Coiled coil;
 KW Alternative splicing.
 FT DOMAIN 13 18 POLY-GLY.
 FT DOMAIN 44 49 POLY-GLU.
 FT ZN_FING 125 154 RING-TYPE.
 FT ZN_FING 212 259 B_BOX-TYPE 1.
 FT ZN_FING 271 312 B_BOX-TYPE 2.
 FT DOMAIN 299 401 COILED COIL (POTENTIAL).
 FT DOMAIN 545 550 POLY-THR.
 FT ZN_FING 887 934 PHD-TYPE.
 FT DOMAIN 974 1046 BROMODOMAIN.
 FT VARSPLIC 1041 1057 Missing (in isoform Beta).
 FT CONFLICT 89 89 /FTIGVSP_005774.
 FT CONFLICT 451 453 V -> E (IN REF. 4).
 FT CONFLICT 909 909 PAA -> LLH (IN REF. 4).
 FT CONFLICT 1037 1037 F -> S (IN REF. 4).
 FT CONFLICT 1114 1127 R -> T (IN REF. 1).
 FT CONFLICT 1114 1127 RKELKSDERPVIK -> QKTPKVR (IN REF. 1).
 SQ SEQUENCE 1127 AA; 122521 MW; 02E3860CFDCFDAB3 CRC64;
 Query Match 52.3%; Score 67.5; DB 1; Length 1127;
 Best Local Similarity 54.2%; Pred. No. 0.013;
 Matches 13; Conservative 6; Mismatches 2; Indels 3; Gaps 1;
 QY 1 FRQVDVAVKGLPDYHKIIKQPMW 24
 DB 982 FQEPVPA---SIPNYKIHKQPMW 1002
 RESULT 15
 GCN5_YEAST STANDARD; PRT; 439 AA.
 ID GCN5_YEAST
 AC Q03330;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Histone methyltransferase GCN5 (EC 2.3.1.48).
 GN GCN5 OR ADAM OR YGR252W.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93011009; PubMed=1396595;
 RA Georgakopoulos T., Thireos G.;
 RT "Two distinct yeast transcriptional activators require the function
 RT of the GCN5 protein to promote normal levels of transcription.";
 RL EMBO J. 11:4145-4152(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97313265; PubMed=9169869;
 RA Tettelin H., Agostoni Carbone M.L., Albermann K., Albers K.,
 RA Arroyo K., Backes U., Barreiros I., Bertani I., Bjorson A.J.,
 RA Brueckner M., Bruschi C.V., Carignani G., Castagnoli L., Cerdan E.,
 RA Clemente M.L., Coblenz A., Coglieva M., Coissac E., Defoor E.,
 RA Del Bino S., Delius H., Delner D., de Wergifosse P., Dujon B.,

RA Durand P., Entian K.-D., Erasos P., Escribano V., Fabiani L.,
RA Fartmann B., Feroli F., Feuermann M., Frontali L., Garcia-Gonzalez M.,
RA Garcia-Gaez M.I., Goffeau A., Guerreiro P., Hani J., Hansen M.,
RA Hebling U., Hernandez K., Heumann K., Hilger F., Hofmann B.,
RA Indge K.J., James C.M., Klima R., Koetter P., Kramer B., Kramer W.,
RA Lauquin G., Leuther H., Louis E.J., Maillier E., Marconi A.,
RA Martegani E., Mazon M.J., Mazzoni C., McReynolds A.D.K.,
RA Melchiorretto P., Mewes H.-W., Minenkova O., Mueller-Auer S.,
RA Nawrocki A., Netter P., Neu R., Nombela C., Oliver S.G., Panzeri L.,
RA Paoluzzi S., Plevani P., Portetelle D., Portillo F., Potier S.,
RA Purnelle B., Rieger M., Riles L., Rinaldi T., Robben J.,
RA Rodriguez-Pousada C., Rodriguez-Belmonte E., Rodriguez-Torres A.M.,
RA Rose M., Ruzi M., Saliola M., Sanchez-Perez M., Schaefer B.,
RA Schaefer M., Schafke M., Schmidheini T., Schreier A., Skala J.,
RA Souciet J.-L., Steensma H.Y., Talla E., Thierry A., Vandenbol M.,
RA van der Aart Q.J.M., Van Dyck L., Vanoni M., Verhasselt P., Voet M.,
RA Volckaert G., Wambutt R., Watson M.D., Weber N., Wedler E., Wedler H.,
RA Wipfler A., Wolf K., Wright L.F., Zaccaria P., Zimmermann M.,
RA Zöllner A., Kleine K.,
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome VII.";
RL Nature 387:81-84(1997).
RN [3]
RP SEQUENCE OF 1-170 FROM N.A.
RC STRAIN=S288C / FY1679;
RX MEDLINE=97279234; PubMed=9133742;
RA Feroli F., Carignani G., Pavanello A., Guerreiro P., Azevedo D.,
RA Rodrigues-Pousada C., Melchiorretto P., Panzeri L.,
RA Agostoni Carbone M.C.,
RT "Analysis of a 17.9 kb region from Saccharomyces cerevisiae
chromosome VII reveals the presence of eight open reading frames,
including BRFL1 (TFR1B70) and GCN5 genes.";
RT Yeast 13:369-372(1997).
RL [4]
RN SEQUENCE OF 170-439 FROM N.A.
RP STRAIN=S288C;
RX MEDLINE=97279233; PubMed=9133741;
RA Mazzoni C., Ruzi M., Rinaldi T., Solinas F., Montebove P.,
RA Frontali L.,
RT "Sequence analysis of a 10.5 kb DNA fragment from the yeast
chromosome VII reveals the presence of three new open reading frames
and of a tRNA^{Thr} gene.";
RL Yeast 13:369-372(1997).
RN [5]
RN ASSOCIATION WITH ADA2.
RX MEDLINE=95045371; PubMed=7957049;
RA Marcus G.A., Silverman N., Berger S.L., Horiuchi J., Guarante L.,
RT "Functional similarity and physical association between GCN5 and
RT ADA2: putative transcriptional adaptors.";
RL EMBO J. 13:4807-4815(1994).
RN [6]
RN IDENTIFICATION IN A SAGA COMPLEX WITH SPT2; SPT7; SPT8; SPT20; HFI1
RP ADA2; ADA3 AND TRAI.
RX MEDLINE=99102959; PubMed=9885573;
RA Grant P.A., Schieltz D., Pray-Grant M.G., Yates J.R. III,
RA Workman J.L.,
RT "The ATM-related cofactor Tra1 is a component of the purified SAGA
RT complex.";
RL Mol. Cell 2:863-867(1998).
RN [7]
RN REVIEW.
RX MEDLINE=20400931; PubMed=10940244;
RA Dyda F., Klein D.C., Hickman A.B.,
RT "GCN5-related N-acetyltransferases: a structural overview.";
RL Annu. Rev. Biophys. Biomol. Struct. 29:81-103(2000).
RN [8]
RN X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 99-262.
RX MEDLINE=99362688; PubMed=10430873;
RA Triebel R.C., Rojas J.R., Sterner D.E., Venkataramani R.N., Wang L.,
RA Zhou J., Allis C.D., Berger S.L., Marmorstein R.,
RT "Crystal structure and mechanism of histone acetylation of the yeast
RT GCN5 transcriptional coactivator.";
RT Proc. Natl. Acad. Sci. U.S.A. 96:8931-8936(1999).
CC -!- FUNCTION: Acetylates Lys-14 of histone H3. Also acetylates Lys-8
and Lys-16 of histone H4 with a lower preference. Acetylation of
histones gives a specific tag for epigenetic transcription
activation. Operates in concert with certain DNA-binding
transcriptional activators such as GCN4 or HAP2/3/4. Acts via the
formation of large multiprotein complexes that modify the
chromatin.
CC -!- CATALYTIC ACTIVITY: Acetyl-CoA + histone = CoA + acetyl-histone.
CC -!- SUBUNIT: Interacts with ADA2. Part of the ADA/GCN5 complex that
consists of HFI1/ADA1, ADA2, ADA3, SPT20/ADAS AND GCN5. Component
of the SAGA complex, at least composed of SPT2, SPT7, SPT8,
SPT20/ADAS, HFI1, ADA2, ADA3/NGG1, TRAI and GCN5.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: Contains 1 bromodomain.
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CC -----
CC EMBL; X68628; CAA48602.1; -;
DR EMBL; Z73037; CAA97281.1; -;
DR EMBL; X99228; CAA67614.1; -;
DR PIR; S28051; S28051.
DR PDB; 1VGH; 02-AUG-99.
DR PDB; 1F6I; 24-NOV-00.
DR GenOnline; 141564; -;
DR TRANSFAC; T02145; -;
DR SGD; S0003484; GCN5.
DR GO; GO:0000124; C:SAGA complex; IDA.
DR InterPro; IPR001487; Bromodomain.
DR InterPro; IPR00182; GCN5acetyl_trans.
DR Pfam; PF00583; Acetyltransf; 1.
DR Pfam; PF00439; bromodomain; 1.
DR PRINTS; PR00503; BROMODOMAIN.
DR SMART; SM00297; BROMO; 1.
DR PROSITE; PS00633; BROMODOMAIN 1; 1.
DR PROSITE; PS0014; BROMODOMAIN 2; 1.
KW Transcription regulation; Transferase; Activator; Chromatin regulator;
KW Trans-acting factor; Nuclear protein; Bromodomain; 3D-structure.
FT ACT_SITE 173 173
FT DOMAIN 344 414
FT STRAND 100 105
FT HELIX 111 127
FT TURN 129 130
FT HELIX 133 141
FT TURN 143 144
FT STRAND 146 152
FT TURN 153 155
FT STRAND 156 166
FT HELIX 167 169
FT TURN 170 170
FT STRAND 171 179
FT TURN 181 182
FT TURN 186 187
FT HELIX 188 203
FT STRAND 208 213
FT HELIX 215 217
FT TURN 218 223
FT TURN 224 225
FT STRAND 227 227
FT HELIX 234 237
FT STRAND 238 238
FT TURN 239 240
FT STRAND 241 241
FT TURN 244 245
FT STRAND 248 253
SQ SEQUENCE 439 AA; 51069 MW; 3200730DDCTEF70D CRC64;
Query Match 47.3%; Score 61; DB 1; Length 439;
Best Local Similarity 54.2%; Pred. No. 0.051;

Matches 13; Conservative 4; Mismatches 5; Indels 2; Gaps 1;

Qy 1 FROPDAVKLGLPDYHKIKQPM 24
Db 352 FLOPVN--KEEVPDYDFIREPMD 373

Search completed: July 27, 2004, 12:07:37
Job time : 15 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 27, 2004, 12:04:47 ; Search time 35 Seconds
(without alignments)
216.355 Million cell updates/sec

Title: US-09-784-553C-19_COPY_29_52
Perfect score: 129
Sequence: 1 FRQPVDAVKGLPDYHKIIKQPM 24

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	129	100.0	503	11 Q99PC5	Q99PC5 mus musculus
2	129	100.0	539	13 Q72VH4	Q72VH4 xenopus lae
3	129	100.0	729	13 Q90971	Q90971 gallus gall
4	129	100.0	798	11 Q8411	Q8411 mus musculus
5	129	100.0	798	11 Q54795	Q54795 mus musculus
6	117	90.7	515	13 Q7SXL8	Q7SXL8 brachydanio
7	113	87.6	1110	5 Q8IRN6	Q8IRN6 drosophila
8	113	87.6	2038	5 Q9W3L3	Q9W3L3 drosophila
9	110	85.3	505	11 Q8C665	Q8C665 mus musculus
10	110	85.3	511	11 Q8CAX7	Q8CAX7 mus musculus
11	110	85.3	556	4 Q8NSM3	Q8NSM3 homo sapien
12	110	85.3	726	11 Q8K2F0	Q8K2F0 mus musculus
13	110	85.3	726	11 Q9J125	Q9J125 mus musculus
14	108	83.7	558	13 Q7SXP6	Q7SXP6 brachydanio
15	107	82.9	723	11 Q8VHF7	Q8VHF7 mus musculus
16	107	82.9	731	4 Q60433	Q60433 homo sapien

ALIGNMENTS

RESULT 1

Q99PC5 PRELIMINARY; PRT; 503 AA.
AC Q99PC5; ID Q99PC5; PRT; 503 AA.
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Ring 3 (Fragment).
GN BRD2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL;
RA Korf I.;
RT "Complete sequence of UL26B06."
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF318183; AAK07919.1; -.
DR HSSP; Q92831; 1B91.
DR MGD; MGI:99495; Brd2.
DR InterPro; IPR001487; Bromodomain.
DR Pfam; PF00439; bromodomain; 2.
DR PRINTS; PR00503; BROMODOMAIN.
DR SMART; SM00297; BROMO; 2.
DR PROSITE; PS00633; BROMODOMAIN_1; 2.
DR PROSITE; PS00633; BROMODOMAIN_2; 2.
FT NON TER 503 503
SQ SEQUENCE 503 AA; 55523 MW; 842A566963981F28 CRC64;

Query Match 100.0%; Score 129; DB 11; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.4e-11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FRQPVDAVKGLPDYHKIIKQPM 24

Db 98 FRQPVDAVKGLPDYHKIIKQPM 121

Q9ESU6 mus musculus
Q8VHF8 mus musculus
Q86YS8 homo sapien
Q8AUM2 oryza lat
Q7SXM5 brachydanio
Q8T3Z6 drosophila
Q9VCG6 grosophila
Q7ZV99 brachydanio
Q8AWX9 brachydanio
Q86S79 caenorhabdi
Q85Y80 caenorhabdi
Q9LY44 mus musculus
Q8QIF7 fugu rubrip
Q76561 caenorhabdi
Q81W16 homo sapien
Q14789 homo sapien
Q7Z4A6 homo sapien
Q8AV32 oryza sativ
Q98711 arabidopsis
Q9GU61 myxine glut
Q8T775 branchiosto
Q7Y214 arabidopsis
Q9LS12 arabidopsis
Q726C1 homo sapien
Q8QZV8 mus musculus
Q9AR00 lycopersico
Q8MTV9 alysia cal
Q8SR93 encephalito
Q9LMU8 arabidopsis

RESULT 2

Q7ZYH4 PRELIMINARY; PRT; 539 AA.
 AC Q7ZYH4
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Similar to bromodomain-containing 2 (Fragment).
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA Klein S., Strausberg R.,
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC043784; AA43784.1; -.
 DR InterPro; IPR001487; Bromodomain.
 DR Pfam; PF00439; bromodomain; 2.
 DR PRINTS; PR00503; BROMODOMAIN.
 DR SMART; SM00297; BROMO; 2.
 DR PROSITE; PS00633; BROMODOMAIN 1; 1.
 DR PROSITE; PS50014; BROMODOMAIN_2; 2.
 FT NON-TER 539
 SQ SEQUENCE 539 AA; 60130 MW; 53841988925415F4 CRC64;

Query Match 100.0%; Score 129; DB 13; Length 539;
 Best Local Similarity 100.0%; Pred. No. 1.5e-11;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FRQPVDAVKLGDPDYHKIIKQPM 24

Db 99 FRQPVDAVKLGDPDYHKIIKQPM 122

RESULT 3

Q90971 PRELIMINARY; PRT; 729 AA.
 AC Q90971
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Kinase.
 DE RING3.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bi2;
 RX MEDLINE=96376536; PubMed=8781126;
 RA Thorpe K.L., Abdulla S., Kaufman J., Trowsdale J., Beck S.;
 RT "Phylogeny and structure of the RING3 gene";
 RL Immunogenetics 44:391-396(1996).
 DR EMBL; X96669; CAA65449.1; -.
 DR HSP; Q92831; IPR01.
 DR InterPro; IPR001487; Bromodomain.
 DR Pfam; PF00439; bromodomain; 2.
 DR PRINTS; PR00503; BROMODOMAIN.
 DR SMART; SM00297; BROMO; 2.
 DR PROSITE; PS00633; BROMODOMAIN 1; 2.
 DR PROSITE; PS50014; BROMODOMAIN_2; 2.
 SQ SEQUENCE 729 AA; 80389 MW; 06E1B92C804DF7B8 CRC64;

Query Match 100.0%; Score 129; DB 13; Length 729;
 Best Local Similarity 100.0%; Pred. No. 2.1e-11;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FRQPVDAVKLGDPDYHKIIKQPM 24
 Db 52 FRQPVDAVKLGDPDYHKIIKQPM 75

RESULT 4

O88411 PRELIMINARY; PRT; 798 AA.
 AC O88411
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Female sterile homeotic-related protein Fig-1.
 GN BRD2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognath.; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Rhee K., Brunori M., Besset V., Wolgemuth D.J.;
 RT "Expression and potential role of Fig-1, a putative murine
 RT bromodomain-containing homologue of the Drosophila gene female sterile
 RT homeotic";
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF045462; AAC24810.1; -.
 DR HSP; Q92831; IPR01.
 DR MGB; MGI:99495; Brd2.
 DR InterPro; IPR001487; Bromodomain.
 DR Pfam; PF00439; bromodomain; 2.
 DR PRINTS; PR00503; BROMODOMAIN.
 DR SMART; SM00297; BROMO; 2.
 DR PROSITE; PS00633; BROMODOMAIN 1; 2.
 DR PROSITE; PS50014; BROMODOMAIN_2; 2.
 SQ SEQUENCE 798 AA; 88063 MW; A9942517CF15B7A1 CRC64;

Query Match 100.0%; Score 129; DB 11; Length 798;
 Best Local Similarity 100.0%; Pred. No. 2.3e-11;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FRQPVDAVKLGDPDYHKIIKQPM 24

Db 98 FRQPVDAVKLGDPDYHKIIKQPM 121

RESULT 5

O54795 PRELIMINARY; PRT; 798 AA.
 ID O54795
 AC O54795
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE RING3 protein.
 GN BRD2 OR RSRG1 OR RING3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognath.; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Thorpe K.L., Beck S.;
 RL Immunogenetics 0:0-0(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129SVJ;
 RA Taniguchi Y., Matsuzaka Y., Fujimoto H., Miyado K., Kohda A.,
 RA Okumura K., Kimura M., Inoko H.;
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 47-549 FROM N.A.
 RC STRAIN=INRED CD-1; TISSUE=Testis;
 RA Taniguchi Y., Matsuzaka Y., Fujimoto H., Miyado K., Kohda A.,
 RA Okumura K., Kimura M., Inoko H.;


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DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Bromodomain-containing 3 (Fragment).
GN BRD3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium.
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
RL ENBL; AK037435; BAC29806.1; -.
RL MGD; MGI:1914632; Brd3.
DR InterPro; IPR001487; Bromodomain.
DR PFAM; PF00439; bromodomain; 2.
DR PRINTS; PR00503; BROMODOMAIN.
DR SMART; SM00297; BROMO; 2.
DR PROSITE; PS00633; BROMODOMAIN_1; 2.
DR PROSITE; PS50014; BROMODOMAIN_2; 2.
FT NON TER 511 511
SQ SEQUENCE 511 AA; 55921 MW; E189A3484AEE2679 CRC64;

Query Match 85.3%; Score 110; DB 11; Length 511;
Best Local Similarity 83.3%; Pred. No. 1.3e-08;
Matches 20; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 FQQPVDAVKLGLPDYHKIIQPMQ 24
DB 58 FQQPVDAIKNLFPDYHKIIKNPMD 81

RESULT 11
Q8N5M3 PRELIMINARY; PRT; 556 AA.
ID Q8N5M3
AC Q8N5M3;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Similar to bromodomain containing 3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR ENBL; BC032124; A8H32124.1; -.
DR InterPro; IPR001487; Bromodomain.
DR PFAM; PF00439; bromodomain; 2.
DR PRINTS; PR00503; BROMODOMAIN.
DR SMART; SM00297; BROMO; 2.
DR PROSITE; PS00633; BROMODOMAIN_1; 2.
DR PROSITE; PS50014; BROMODOMAIN_2; 2.
SQ SEQUENCE 556 AA; 60942 MW; 8352F5DF1801A793 CRC64;

Query Match 85.3%; Score 110; DB 4; Length 556;
Best Local Similarity 83.3%; Pred. No. 1.5e-08;
Matches 20; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 FQQPVDAVKLGLPDYHKIIQPMQ 24
DB 59 FQQPVDAIKNLFPDYHKIIKNPMD 82

RESULT 12
O8K2F0

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ID Q8K2F0 PRELIMINARY; PRT; 726 AA.
AC Q8K2F0;
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Bromodomain-containing 3.
GN BRD3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC015366; AAH31536.1; -.
DR MGD; MG1:1914632; Brd3.
DR InterPro; IPR001487; Bromodomain.
DR Pfam; PF00439; bromodomain; 2.
DR PRINTS; PR00503; bromodomain.
DR SMART; SM00297; BROMO; 2.
DR PROSITE; PS00633; BROMODOMAIN_1; 2.
DR PROSITE; PS00633; BROMODOMAIN_2; 2.
DR PROSITE; PS00614; BROMODOMAIN_2; 2.
SQ SEQUENCE 726 AA; 79791 MW; 4BC2FC0ACA41D5CD CRC64;

Query Match 85.3%; Score 110; DB 11; Length 726;
Best Local Similarity 83.3%; Pred. No. 2e-08;
Matches 20; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 FRQPDVAVKLGPDYHKIKQPM 24
| : : : : : : : : : : : : : : : :
DB 58 FYQFVDAIKLNPYHKIKQPM 81

RESULT 13
Q9J125 PRELIMINARY; PRT; 726 AA.
AC Q9J125;
DT 01-OCT-2000 (T-EMBLrel. 15, Created)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Bromodomain-containing FSH-like protein FSRG2.
GN BRD3 OR 2410084F24IK OR FSRG2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Shang E., Wolgemuth D.J.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF269193; AAF78072.1; -.
DR HSP; Q92831; I891.
DR MGD; MG1:1914632; Brd3.
DR InterPro; IPR001487; Bromodomain.
DR Pfam; PF00439; bromodomain; 2.
DR PRINTS; PR00503; BROMODOMAIN.
DR SMART; SM00297; BROMO; 2.
DR PROSITE; PS00633; BROMODOMAIN_1; 2.
DR PROSITE; PS00633; BROMODOMAIN_2; 2.
DR PROSITE; PS00614; BROMODOMAIN_2; 2.
SQ SEQUENCE 726 AA; 79745 MW; 7AB3B4DAD38A78F4 CRC64;

Query Match 85.3%; Score 110; DB 11; Length 726;
Best Local Similarity 83.3%; Pred. No. 2e-08;
Matches 20; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 FRQPDVAVKLGPDYHKIKQPM 24
| : : : : : : : : : : : : : : : :
DB 58 FYQFVDAIKLNPYHKIKQPM 81

RESULT 14
Q7SXP6 PRELIMINARY; PRT; 558 AA.
AC Q7SXP6;
DT 01-OCT-2003 (T-EMBLrel. 25, Created)
DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
CX Cyprinidae; Danio.
CX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=AB; TISSUE=Body;
RL MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Woxley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RL "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=AB; TISSUE=Body;
RA Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC055508; AAH55508.1; -.
KW Hypothetical protein.
FT NON TER 558 558
SQ SEQUENCE 558 AA; 62059 MW; 61681C83FBB8FA3D CRC64;

Query Match 83.7%; Score 108; DB 13; Length 558;
Best Local Similarity 79.2%; Pred. No. 3e-08;
Matches 19; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 FRQPDVAVKLGPDYHKIKQPM 24
| : : : : : : : : : : : : : : : :
DB 73 FHEPVDATLNLDPYHKIKQPM 96

RESULT 15
Q8VHF7 PRELIMINARY; PRT; 723 AA.
AC Q8VHF7;
DT 01-MAR-2002 (T-EMBLrel. 20, Created)
DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Bromodomain-containing protein BRD4 short variant.
GN BRD4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

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RA Houzelstein D., Bullock S.L., Lynch D.E., Grigorieva E.F.,
RA Wilson V.A., Beddington R.S.P.;
RT "Growth and early post implantation defects in mice mutant for the
RT bromodomain-containing protein Brd4.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF461396; AAL67834.1; -.
DR InterPro; IPR001487; Bromodomain.
DR Pfam; PF00439; bromodomain; 2.
DR PRINTS; PR00503; BROMODOMAIN.
DR SMART; SM00297; BROMO; 2.
DR PROSITE; PS00633; BROMODOMAIN_1; 1.
DR PROSITE; PS00014; BROMODOMAIN_2; 2.
SQ SEQUENCE 723 AA; 80635 MW; 738F2AE5F58A56BC CRC64;

Query Match 82.9%; Score 107; DB 11; Length 723;
Best Local Similarity 83.3%; Pred. No. 5.8e-08;
Matches 20; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 FRQPVDAVLGLPDYHKIIKQPMQ 24
Db 83 FQGPVDAVLNLDPYKIKIKTPMD 106

Search completed: July 27, 2004, 12:08:24
Job time : 36 secs

